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APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 00/092,155
SOFTWARE: PatentIN Ver. 2.0
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US-09-817-180-3

US-08-884-324-14

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NAME/KEY: unsure

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OTHER INFORMATION: N

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US-09-033-333-2

US-09-103-145-17

US-09-103-131-1

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APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Dayster, Lyn M
APPLICANT: Evustaci, Jana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENT ON NUMBER: 60/092,155
SOFTWARE: PATENTING DATE: 1998-07-09
SERLIER PILING DATE: 1998-07-09
SOFTWARE: PATENTING DATE: 1998-07-09
SOFTWARE: PATENTING DATE: 1998-07-09
SOFTWARE: PATENTING DATE: 1998-07-09
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                                                                                                                            Sequence 7, Application US/09146580A Patent No. 6306653
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LOCATION: (272)
S. OTHER INFORMATION: N at position
US-09-146-580-7
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Matches 379; Conservative
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FEATURE:
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ENGTH: 381
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Fatent No. 6306633

GENERAL INFORMATION:
APPLICANT: Pastdero, Lawrence D
APPLICANT: Pastdero, Lawrence D
APPLICANT: Frustaci, Jana M
TILE REFERENCE: 200755/1002
CURRENT FILING DATE: 1998-09-03
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/091,889
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-20
SOFTWARE OF SEQ ID NOS: 18
SOFTWARE PATENTING DATE: 1998-01-09
SOFTWARE: BALENTING DATE: 1998-01-09
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Parent No. 6306653
GREAT INFORMATION:
APPLICANT: Papsidero, Lawrence D
APPLICANT: Pyster, Lyn M
APPLICANT: Frustaci, Jan M
TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
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Pred. No. 1.4e-77;
0; Mismatches 2; Indels
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COTHER INFORMATION: N at position 162 is either A, US-09-146-580-11
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Best Local Similarity 99.3%;
Matches 302; Conservative (
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OTHER INFORMATION: N
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Gaps
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                                                                                    2.6%; Score 52; DB 4; Length 5835; 100.0%; Pred. No. 2.3e-13; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.3e-13;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Calydon, Inc.
TITLE OF INVENTION: Tissue-Specific Enhancer Active in TITLE OF INVENTION: Prostrate
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcardero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTAM I.
REGISTRATION NUMBER: 20015
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/380,916
FILING DATE: 12-JAN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08380916
Patent No. 5648478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08721690; Patent No. 6057299; GENERAL INFORMATION: APPLICANT: Henderson, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-380-916-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS: . LENGTH: 5836 base pairs
                                                                                                                            52; Conservative
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Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                         Best Local Similarity
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US-09-033-333-3
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US-08-380-916-1
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US-08-721-690-1
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STATE:
                                                                                      Query Match
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                                                                                                                            Matches
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APPLICANT: Yu, De Chao

APPLICANT: Schuur, Eric

APPLICANT: Schuur, Eric

APPLICANT: Henderson, Daniel

TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC

TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE

TITLE OF INVENTION: 14 PREROF

NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                           Score 104; DB 4; Lv
Pred. No. 1.5e-35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FeatsED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER FILING DATE: 1998-01-09
EARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                            Query Match 5.2%; Score 104; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 104; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFLLING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION UNBER: 40,130
REFERNCE/DOCKET NUMBER: 3480;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09033333 Patent No. 6197293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: 650.
TELERAX: 706141
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5835 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-146-580-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                   SEQ ID NO 8
LENGTH: 104
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                                                                                                                                                                                                                               TYPE: DNA
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APPLICANT: Yu, De Chao
APPLICANT: Yu, Eric
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
APPLICANT: APPLICANTION: THEREOF
AUTHE OF INVENTION: THEREOF
AUTHE OF INVENTION: THEREOF
AUTHERSON OF USE
ADDRESSE: MORRISON & FOERSTER
ADDRESSE: MORRISON & FOERSTER
ATREET: 755 PAGE MILL ROAD
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.6%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 52; Conservative 0; Mismatches
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                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/380,916
FILING DATE: 30-7AN-1995
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 34802-20001
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-033-333-2; Sequence 2, Application US/09033333; Patent No. 6197293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 3480
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                TELEFAX: 415-494-0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: S816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-891-581-1
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APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: ITSSUE SPECIFIC ENHANCER ACTIVE
TITLE OF INVENTION: IN PROSTATE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
      TISSUE-SPECIFIC ENHANCER ACTIVE IN PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 52; DB 3; Ler
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                            COMPUTER: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,690
FILING DATE: 37-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/380,916
FILING DATE: 30-JAN-1995
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REFISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 40,130
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FSSLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TISSUE-SPECIFIC TITLE OF INVENTION: IN PROSTATE NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSE: MORRISON & FOERSTER STREET: 75 PAGE MILL ROAD CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08891581
Patent No. 6136792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5836 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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US-08-891-581-1
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Gaps

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RESULT 12
US-08-611-587-1/c
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0
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                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6%; Score 52; DB 4; Length 5836;
100.0%; Pred. No. 2.3e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8453;
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io. 6e-13;
0; Indels
                                                                                                                                                                                                                                                                                      Sequence 45, Application US/09167681A

Patent No. 6265561

GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Dianne M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
2.5%; Score 51; DB
Best Local Similarity 100.0%; Pred. No. 6e-
Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 45 LENGTH: 8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bozicevic & Reed, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09009913
Patent No. 6087485
LENGTH: 5836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                Query Match
Best Local Similarity 100.(
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS (6322)...(6447)
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(4827)...(4925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                 STRANDEDNESS: SIT
TOPOLOGY: Linear
US-09-033-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                RESULT 10
US-09-167-681-45
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US-09-009-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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Gaps
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APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLTO, MARIA D.
APPLICANT: MOLTO, MARIA D.
APPLICANT: Campuzano, Victoria
APPLICANT: Cossee, Mireille
TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept. STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 3;
Pred. No. 7.4e-11
                                                                                                                              SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Sco. 100.0%; Pred. No. ...
285 Hamilton Ave, Suite 200
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APPLICATION NUMBER: US/08/611,587
FILLING DATE: 03-MAR-1996
CLASSIFCATION: 436
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SE
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: 650-327-3231
                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 72928 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-009-913-1
                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.3
Best Local Similarity 100.
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                 Palo Alto
                                                     USA
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STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                 STATE: CA
COUNTRY: U
                                                                       94301
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us-09-813-492-1.oli.rni

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APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Brichard, Vincent; Van Pel, Thomas; Coulle, Pierre;
APPLICANT: Traversari, Catia; W lfel, Thomas; Coulle, Pierre;
APPLICANT: Traversari, Catia; W lfel, Thomas; Coulle, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaen, Ettenne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES:
ADDRESSE:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
2.1F: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.2%; Score 44; DB 2; Lu
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 44; Conservative 0; Mismatches 0;
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REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
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APPLICATION NUMBER: US/08/370,319
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APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
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US-09-224-834-12/c
Sequence 12, Application US/09224834
Patent No. 6201111
GENERAL INFORMATION:
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TELEFAX: (212) 638-3864
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TELEPHONE: (212) 688-9200
TELEFAX: (212) 888-3884
INFORMATION FOR SEQ. ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  (212) 688-9200
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FDNESS: double
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New York
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-370-319C-12
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Patent No. 5856091

GENERAL INFORMATION:
APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W 1fel, Thomas; Coulie, Pierre;
TITLE OF INVENTION: ISOLATED NUCLEEC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%; Score 45; DB 3; Ler 100.0%; Pred. No. 2.3e-10; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319C
FILING DATE: 10-JANUARY-1995
CLASSIFCATION: 435
                                 Sarah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5856091man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,351
FILING DATE: 8 JULY-1994
PRIOR APPLICATION NUMBER: 08/032,978
                                                                          REFERENCE/DOCKET NUMBER: D-59
TELECOMUNICATION INFORMATION:
TELEPHONE: 713-651-520
TELEFAX: 76-2829
INFORMATION FOR SEQ 10: 5EQUENCE CHARACTERISTICS:
LENGTH: 8353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                 NAME: Brashears-Macatee, Sa REGISTRATION NUMBER: 38,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 9q13
       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.2%
Best Local Similarity 100.0
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: 1
ANTI-SENSE: NO
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Factor 15.3-11/C54
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PELING DATE: 1999-00-02
SARLIER PELING DATE: 1997-08-04
NUMBER OF SEQ ID NOWE: 18
SOFTWARE: FASTEEQ for Windows Version 3.0
SEQ ID NO 17
TANGORY TANGO TANGORY TANGORY
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; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3 ; OTHER INFORMATION: kilobases US-09-224-834-12
                                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 44; DB 4; Length 4129; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 44; Conservative 0; Mismatches 0; Indels
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LOCATION: (1)...(176373)

COTHER INFORMATION: n = A,T,C or G

US-09-128-155-17
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US-09-128-155-17/c
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Search completed: October 7, 2002, 12:56:52 Job time: 6736 sec

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Human reproductive
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Human reproductive
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secreted pro
                              DNA encoding novel
Human breast speci
Human secreted pro
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Human C-C chemokin
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Human immune/haema
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immune/haema
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AAL05517
AAL05518
AAK87363
AAK87360
AAK87354
AAK87355
AAK87354
AAK87354
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AAV38292
AAS81261
AAK75733
ABA18403
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AAK86144
AAK84160
AAK79161
ABA08089
AAL06868
AAS30459
AAC02850
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AAC21190
AAX98284
         AAC89722
AAX89394
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56..439
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96US-0031805
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56..121
/*tag= b
122..436
/*tag= c
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Homo sapiens
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27-NOV-1996;
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RESULT
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                                                                                                                                                                                                        This cDNA sequence codes for human DNAX Vic-1 (DVic-1) (see AAW60649), a novel C-C chemokine. DVic-1 cDNA can be obtained from e.g. skin, epithelial or wound healing libraries by PCR amplification or by hybridisation. 2 ESTS (see AAV38292-93) were obtained from a human foetal heart library and a human osteoblast library. These show compared, and are probably ESTS from a similar transcript. The chemokine motifs of these 2 ESTS were compared, and a consensus sequence was derived and confirmed as encoding DVic-1. The DVic-1 gene has been localised to human chromosome 9p13. An alternative in onger transcript (see AAV38296) for human DVic-1 is also disclosed. Also claimed is novel human DNAX Groin Wound expressed CC chemokine (DGWCC) (see AAW60649), as well as expression vectors and host cells.
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                                                                                                treating abnormal physiology or development, e.g. cancerous or degenerative conditions
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100.0%; Pred. No. 1.2e-193;
ive 0; Mismatches 0;
                                Vicari A, 2lotnik A;
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(SCHE ) SCHERING CORP
                                Morales
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Modulating cell movement within the skin, useful for treating immunological skin conditions or diseases comprises administering T cell-attracting chemokine or vasoactive intestinal contractor chemokine
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Human; G-protein coupled receptor; GPR27; antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian; cardiant; hypertensive; hypotensive; diuretic; osteopathic; antiulcer; cerebroprotective; antiallergic; antiemetic; tranquilliser; nootropic; antidepressant; neuroleptic; anticonvulsant; vaccine; gene therapy; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic disorder; neurological disorder; dyskinesia; ss.
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Integrated GPR27. GPR27 has antimidrophial, analgasic, cytostatic, antidiabetic, ancectic, antiasthmatic, antiparkinsonian, cardiant, hypotensiave, diuretic, osteopathic, cerebroprotective, antidiabetic, antidiabetic, antidepressant, antidepressant, neuroleptic, nootropic and anticonvulsant activities, and can be used in producing vaccines and in gene therapy. The GPR27 protein and polynucleotide are useful for treating certain diseases or as vaccines against these diseases. These diseases include bacterial, fungal, proteins are useful for treating certain diseases or as vaccines against these diseases. These diseases include bacterial, fungal, proteocoan or viral (e.g. infections caused by HIV-1 or HIV-2) infections, pain, cancers, diabetes, obesity, anorexia, bulinia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary cretention, osteoprorsis, anglian pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders (e.g. anxiety, schizophrenia, manic depression, depression, delirium, dementia or mental retardation), or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's sydrome). The polynuchectide may also be used for chromosome
                              upled receptor GPR27 polypeptides and polynucleotides, as or for treating diseases, e.g. infections, pain, retention, osteoporosis, stroke, psychotic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic reagent for detecting mutations in the associated gene.
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                                                                                                                                                         present sequence encodes a human G-protein coupled receptor
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100.0%; Pred. No. 1.2e-193
ive 0; Mismatches 0;
                                                                                                                       Page 29; 31pp; English.
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                                                                                      neurological disorders
                                New G-protein coupled
useful as vaccines or
cancers, urinary reten
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AAB69175.
                                                                                                                       Claim 2;
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WPI; 2001-457603/49.
P-PSDB; AAM25479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. And P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P carperssion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing that the nucleic acids into a host cell and culturing the cell of or express the proteins. N and P can be used in the prevention, diagnosis and ABB7789 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1471 agttgataccattgtgccattcctcttttggcctcttttttgtccatagaggcttcaaga 1530
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                                                                                                                                                                                                      colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.5%; Score 434; DB 22; Length 643; 99.6%; Pred. No. 1.6e-167; ive 0; Mismatches 2; Indels
                                                                                                                                                                  Human colon cancer antigen encoding cDNA SEQ ID NO:1184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 643 BP; 210 A; 117 C; 116 G; 198 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2980-2981; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birse CE,
                                                   AAH34102 standard; cDNA; 643 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0157137.
                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US26524
                                                                                                                              (first entry)
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Matches 534; Conservative
                                                                                                                                                                                                                       colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-235357/24.
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                                                                                                                                                                                                                                                                                              WO200122920-A2.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1999;
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                                                                                                                            03-SEP-2001
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                                                                                       AAH34102;
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                                  AAH34102
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antificiammatory; antirheumatic; antiarthritic; immunosuppressive;
w antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anamiagentic; antianiaemic; antianaemic; anti-HIV; fungicide; antianiaemy; cardiovascular; antianaemic; eczema;
w dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
w dermatological; antidepressan; nootropic; antidiabetic; cytostatic;
w numnostimulant; gene therapy; antisense therapy; vaccine; inflammation;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancratitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autolumnunity;
genetic disease; haematopoletic disorder; platelet disorder; asthma;
w hirombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; disbetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
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                                                                                     atgtcttggaggtgataatgggacacacagaggcactgagtctccataggttaaaatgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein encoding cDNA sequence SEQ ID NO:255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH99420 standard; cDNA; 698
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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AAX40376 standard; cDNA; 383

(first

16-JUN-1999

AAX40376:

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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antinheumatic; cells they are expressed in, such as: antinflammatory; antinheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; antianaemic; antiaggregant; haemostatic; vulnerary; antidiabetic; osteopathic; antiaggregant; haemostatic; uninerary; antidiabetic; cytostatic; neuroprotective; antidiabetic; uninerary; antidiabetic; cytostatic; neuroprotective; antidiabetic; osteopathic; dermatological; antidiabetic; antidiabetic; optostatic; neuroprotective; antidiasematic; antidiabetic; osteopathic; dermatological; antidiabetic; osteopathic; dermatological; antidiaperessant; nootropic; antidiabetic; cytostatic; neuroprotective; antidiaperessant; nootropic; conding them can be used in gene therapy antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for conding arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, canaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, costeoporosis, severe combined immunodeficiency, eczema, allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             depression,
            polypeptides, useful for
ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis, severe combined immunodeficiency, eczema, allergir
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depress.
Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 698 BP; 172 A; 170 C; 188 G; 168 T; 0 other;
polynucleotides encoding
                                        treatment and diagnosis of e.g. cancer,
                                                                                                    English.
                                                                                             1217pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorders.
         Isolated
                                                                                                 Claim
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Gaps ö Length 698; Indels Score 403; DB 22; Pred. No. 7.3e-155; Mismatches , 0 20.0%; 503; Conservative Similarity

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203 180 240 300 443 503 480 ctgttaagcagtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgcc 360 9 gaaggotcotggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgact tggctgctgtcatccttcatgtcaagcgcagaagaatctgtgtcagcccgcacaaccata ctgttaagcagtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgcc acaggaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaa catacggccataaaactccttattagagagtctacagataaatctacagagacaattcct cagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttcca acaggaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaa caagtggacttggccatgattggtt 588 Query Match Best Local S Matches 144 19 121 264 181 241 444 361 504 84 204 324 384 301 421 564 481 셤 ô g ò 셤 ô g õ a õ g ò a ò a ò g

human secreted proteins, and encode the proteins given in AAY1531 to human secreted proteins, and encode the proteins given in AAY11533 to AAY11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted human gene products. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, hemotopies regulating activity, tissue growth regulating activity, hemotopies activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping prometer sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. haemostatic; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; hematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat thrombolytic; anti-inflammatory; tumour inhibition; ds. New nucleic acids encoding human secreted proteins - obtained from CDNA libraries derived from liver, lung, large intestine, colon, secreted protein; EST; expressed sequence tag; diagnosis; Sequence 383 BP; 101 A; 91 C; 104 G; 87 T; 0 other; Lacroix B; Human secreted protein 5' EST SEQ ID NO:163 Claim 1; Page 276-277; 398pp; English. ٦, Duclert A, Dumas Milne Edwards 98WO-IB01233. 97US-0904468 thyroid and pancreas tissue WPI; 1999-153700/13. P-PSDB; AAY11658 (GEST) GENSET Homo sapiens. WO9906439-A2. 31-JUL-1998; 01-AUG-1997; 11-FEB-1999

ö 207 gcagcagagagactcgccatcgtggccttggctgtctgtgcggccctacatgcctcaga 121 Gaps 61 gcagcagagagactcgccatcgtggccttggctgtctgtgcggccctacatgcctcaga agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag ö Length 383; Indels 18.9%; Score 382; DB 20; L Llarity 100.0%; Pred. No. 2.9e-146; Conservative 0; Mismatches 0; Similarity Matches 382; Query Match Local 88 148 62 õ g δλ ద

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13-FEB-2002
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                                                                                                                                                                  Matches 432;
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                                                                                                                                                 Query Match
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AAS76558/c
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                                                                                                                                                                                                                                                              breast tumour; CC chemokine; hTECK homologue; developmental disorder; cell proliferative disorder; immune disorder; reproductive disorder; cardiovascular disorder; bacterimal infection; viral; fungal; parasitic; cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents cDNA encoding human growth factor related molecule GFRP-2. cDNA encoding GFRP-1 was initially identified in a breast tissue cDNA library, and the present sequence represents a consensus derived from several overlapping and/or extended cDNA clones. GFRP-2 is probably a CC chemokine and has chemical and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human growth factor related molecule protein useful for the diagnosis and treatment of disorders associated with its activity including developmental, cell proliferative, immune, reproductive and cardiovascular disorders and infections -
                327
                                 241
                                                   387
                                                                   301
                                                                                     447
                                                                                                      361
181
                                                  agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag
                  gctcctggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttggc
                          Baughn MR;
                                                                                                                                                                                                                                                       Human GFRP-2; growth factor related molecule; breast tissue;
                                                                                                                                                                                                                                      cDNA encoding human growth factor related molecule GFRP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NC,
                                                                                                                                                                                                                                                                                                                                                             /product- "Human GFRP-2"
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                                                                                                                        469
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                                                                                                                                       362 gaagaaacaccatggcaagagg 383
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                                                                                                                                                                                  AAA52456 standard; cDNA; 566
                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0181711.
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99US-0313457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 74; 80pp;
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                                                                                                                                                                                                                                                                                                 consensus; ss
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1999;
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Au-Young
                                                                                                                                                                                                    AAA52456;
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                                 182
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                 268
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homology with hTECK (20% identity). GFRP-2 and hTECK are both basic proteins, having isoelectric points of 10.1 and 10.2, respectively. GFRP-2 was found by Northern analysis to be expressed in both tumorous and nontumorous breast tissue. GFRP proteins (AAB03000-B03003), nucleotides encoding them (AAA52455-A52458), GFRP agonists and antagonists may be used to treat a wide variety of diseases associated with increased or decreased expression or activity of GFRP proteins. Conditions which may be treated include developmental disorders, cell proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., menstrual cycle disorders) cardiovascular disorders (e.g., arteriosclerosis) and bacterial, viral, fungal or parasitic infections. Additionally, GFRP proteins and nucleotides can be used in the diagnosis of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggactegecategtggeettggetgtetgtgeggeettacatgeetcagaagecatact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 382; DB 21;
Pred. No. 2.8e-146;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.9%;
99.8%;
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Query Match
Best Local Similarity 100.C
Matches 313; Conservative
                                                AAX89389;
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              AAX89389
                                      The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conditional coding sequences of the invention.

Calagnostics coding sequences of the invention.

Calagnostic coding sequences of the invention.

Calagnostic coding sequence of the invention.

Calagnostic coding sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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100.0%; Pred. No. 1.6e-127;
tive 0; Mismatches 0;
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                                                                                                                                                                                                             Claim 1; SEQ ID No 12362; 103pp; English.
                                                                                    Tang YT;
30-MAR-2001; 2001WO-US08631
                        31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                          WPI; 2001-639362/73.
P-PSDB; ABG12371.
                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 336; Conserv
                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                      biodiversity
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antibonize peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antiponic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding cystitis, and benign hyperplasias as well as other malignancies. The present sequence represents the nucleotide sequence of the human mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A mammary associated chemokine and related polynucleotides, useful for detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                           Chemokine, breast tissue, breast milk, breast disease, vaccine, liflammation, infection, mastitis, benign cystitis, hyperplasia; mammary associated chemokine; MACK; ss.
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Xaa)
                                                                                                                                                                                    Human mammary associated chemokine (MACK) encoding cDNA.
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/transl_except= (pos: 254..256,
/transl_except= (pos: 317..319,
/product= "MACK"
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/note= "Xaa = unknown"
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AAX89389 standard; cDNA; 3117
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116..430
/*tag= c
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Length 3117; Indels 697 ctcaaactcctgggctcaagcgatcctcccaccttagcctcccaaagtactgggattata 756

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15.5%; Score 313; DB 20; I 100.0%; Pred. No. 3.4e-118; ive 0; Mismatches 0;

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detection and treatment of breast disease, especially cancer
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                   tttgagtagctaccgttgtttggattgaaattttctgatactgaaaaagaacaaaaagcct
                                                                                                                                                                                                                                                                                                  Xaa = unknown; the start and stop codons
are not indicated"
                                                                                                                                                                                                                Chemokine; breast tissue; breast milk; breast disease; vaccine; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; ss.
                                                                                                                                                                                                     Human mammary associated chemokine (MACK) open reading frame.
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/transl_except= (pos: 270..272, aa: Xaa)
/product= "MACK"
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69..378
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/codon_start= 3
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98US-0071899.
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P-PSDB; AAY29092, AAY29093.
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20-JAN-1998;
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antigody that recognizes the novel chemokine, or a chemokine-derived antigonic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antigonic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine can samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding polynucleotides include inflammations, infections, mastitis, benign polynucleotides include inflammations, infections, mastitis, benign present sequence represents the human manmary associated chemokine present sequence.

(MACK) open reading frame sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagccatacttcccattgcctccagctgttgcacgaggtttcacatcatatttccagaa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacat 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 aagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ggaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacat 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttaagcagtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 381 BP; 110 A; 91 C; 97 G; 81 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 279; DB 20;
Pred. No. 3.1e-104;
0; Mismatches 2;
Claim 20; Page 20; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Sco.
larity 99.5%; Pro.
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 acggccataaaactccttatt 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC89722 standard; cDNA; 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 acggccataaaactccttatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human RinTinTin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antigenic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a callular receptor for the chemokine, can also be used to treat breast disease. Antigenic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding polynucleotides include inflammations, infections, mastitis, benign cystitis, and benign hyperplasias as well as other malignancies. The present sequence represents an antisense riboprobe that hybridises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 tgctgtcatccttcatgtcaagcgcagaagaatctgtgtcagcccgcacaaccatactgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taagcagtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 gaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A mammary associated chemokine and related polynucleotides, usef for detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the human mammary associated chemokine (MACK) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 311 BP; 65 A; 77 C; 72 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.0%; Score 202; DB 20; Best Local Similarity 99.3%; Pred. No. 8.4e-73; Matches 302; Conservative 0; Mismatches 2;
                                                                                                                                                                                         Papsidero LD;
                                                                                                                                                                                                                                                                                                                           Claim 29; Page 26; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS81262 standard; cDNA; 474 BP.
                                                                                                                                                  (CODO-) CODON DIAGNOSTICS LLC
                                                                                        98US-0092155.
98US-0071899.
                                                      99WO-US00651
                                                                                                                                                                                         Frustaci JM,
                                                                                                                                                                                                                             WPI; 1999-458469/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 cggc 511
                                                    12-JAN-1999;
                                                                                                              20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                22-JUL-1999
                                                                                                                                                                                         Dyster LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 CGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS81262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine; breast tissue; breast milk; breast disease; vaccine; human; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; probe; ss.
                                                                                                                                                                                                                                                                                                   Rin tin tin polypeptides and polynucleotides useful as a diagnostic tool and for treating and preventing various diseases e.g. autoimmune diseases, cancer, infections, bone disorders etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 atgcagcagagagactcgccatcgtggctttggctgtcttgcggccctacatgcctca 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rintintin polynucleotide is useful as a diagnostic reagent through detecting mutations in the associated gene. The polynucleotide and polypeptide are useful for screening agonists and antagonists of Rintintin and are also useful as vaccines in treating various diseases, such as allergies, asthma, atherosclerosis, autoimmune disease, cancer, osteoarthritis, various infections, psoriasis, rheumatoid arthritis, and vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a chemokine designated RinTinTin. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 gctgctgtcatccttcatgtcaagcgcagaagaatctgtgt 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 294 BP; 72 A; 71 C; 81 G; 70 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 221; DB 22;
Pred. No. 1.5e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score ___ 100.0%; Pred. No. 1.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MACK hybridising antisense riboprobe.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 27; 30pp; English.
                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX89394 standard; DNA; 311 BP
                                                                                        24-MAY-2000; 2000WO-US14197
                                                                                                                            99US-0321651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 221; Conservative
                                                                                                                                                                                                         Vawter L;
                                                                                                                                                                                                                                           WPI; 2001-061533/07.
P-PSDB; AAB50353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
            WO200073447-A1.
                                                                                                                                                                                                         Appelbaum E,
                                                                                                                            28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                  07-DEC-2000
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ID AAX893
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Gaps

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Length 311; Indels 327 192 387 132 447 507

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Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific genes -
                                                                                                                                                                                                                                                                                           Human; breast specific gene; breast specific marker; BSG; dlagnosis;
                                                                                                                                                                                                                                                     Human breast specific gene LS clone 2299454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 41; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recipon H, Cafferkey R;
                                                                                                                                   AAZ91767 standard; DNA; 253 BP.
                                                                                                                                                                                                                                                                                                                  breast cancer; therapy; ss
(DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-205737/18.
                                                                                                                                                                                                                                                                                                                                                                                           WO200008210-A1.
                                                                                                                                                                                                              01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1999;
                                                                                                                                                                            AAZ91767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AsS64197-AsS4564 represent novel human amino acid sequences. AsS64197-AsS4564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 474 BP; 134 A; 112 C; 124 G; 104 T; 0 other;
                                      encoding novel human diagnostic protein #17066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 192; DB 23;
100.0%; Pred. No. 9.8e-69;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 17066; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Tang YT
                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                           Ormanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG17075
                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 blodiversity
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                              11-OCT-2001
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Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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98US-0095232.

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This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, imaging and treating breast cancer (BC). The methods comprise measuring the alto comparing the measured levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gactogccatcgtggccttggctgtctgtgcggccctacatgcctcagaagccatacttc 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 gactcgccatcgtggccttggctgtctgtgcggccctacatgcctcagaagccatacttc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                       cytotoxic agent, and used for treating BC in a patient.
                                                                                                                                                                                                                                                                                             Sequence 253 BP; 52 A; 64 C; 70 G; 60 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 180; DB 21;
.00.0%; Pred. No. 8.2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%; Pi
مرثح مرث
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX51656 standard; cDNA; 254
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ID AAX5:
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AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12681 to AAX12913. respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, coll proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, receptor/ ligand activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a
                                                                                                                                    Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; hacmatopoiesis regulation; tissue growth regulation; reproductive hormone requiation; chemotactic; chemokinetic; hacmostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide into a membrane, or importing a polypeptide into a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                              Human secreted protein 5' EST SEQ ID NO:235.
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                  AAX51656;
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÷ Gaps ; 0 Length 254; Indels .; O 6.2%; Score 126; DB 20; 100.0%; Pred. No. 8.9e-42; Live 0; Mismatches 0; Best Local Similarity 100.0 Matches 126; Conservative Similarity Query Match

Sequence 254 BP; 55 A; 72 C; 64 G; 62 T; 1 other;

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101 5.0 230 9 BED04103 BED04103 BED04103 CMO-BN010 98 4.9 454 12 AQ483825 AQ575795 AQ575795 AQ575795 AQ575795 AQ575795 AQ728859 BC775795 AQ728859 BC742439 BC742439 BC742439 BC742439 BC742439 BC728659 BC72464_B BC7249748 BC1240725 BC1 BC1025 BC1025 BC1 BC1025 BC1 BC1025 BC1025<	2.9 460 10 BF914859 2.8 326 12 AF101547 2.8 436 12 AQ412502 2.8 524 10 BF865511 2.8 562 10 BF865511 2.8 569 10 BF838015	2.8 636 12 AGB89464 2.8 491 12 AGD8324 2.8 530 12 AGD57885 2.8 1056 10 BM470567	2.7 478 10 BF748242 2.7 300 9 AW842919 2.7 439 12 A0009550 2.7 546 12 A0393319 2.7 567 12 A056351 2.7 507 10 BF330483	2.7 1140 10 BG389076 BG389076	ALIGNMENTS BF034600 698 bp mRNA linear EST 20-OCT-2000 601455024Fl NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859036 5', mRNA sequence.	BF034600.1 GI:10742312 EST. Hounan. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	Tissue Procurement: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be Clone distribution: MGC clone distribution information can be	http://image.lnl.gov Plate: LLAM9591 row: o column: 05 High quality sequence stop: 698. Location/Qualifiers Location/Qualifiers l. 698 /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="liMGE:3859036" /tissue_type="adenocarcinoma" /tas_bost="DH10B (phage-resistant)" /note="Ordan: oraxiv: vocator: pCMM-SDOPM6. Site 1: Not1:	Site_2: Sall, Cloned unidirectionally. Primer: 011go dT. Average insert size 1.8 kb. Library constructed by Life Technologies. 7
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compuent (c) 1993 - 2000 Compuent (c) 1993 - 2000 Compuent (c) 1993 - 2000, 09:36:05; Searcotober 7, 2002, 09	US-09-813-492-1 2017 1 tagatacctgaacacctcca* OLIGO_NUC Gapop 60.0 , Gapext 60.0	13736207 seqs, 6748477542 residues 0	f hits satisfying chosen parameters: length: 0 length: 2000000000	Listing first 45 summaries	EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 5: em_estin:* 6: em_estov:* 6: em_estpl:* 7: em_estro:* 8: em_tc:* 9: gb_est1:*	10: gb_est2:* 11: gb_ftc:* 12: gb_gss:* 13: em_gss_hum:* 14: em_gss_liv:* 15: em_gss_liv:* 16: em_gss_vtt:*	No. is the number of results predicted greater than or equal to the score of a derived by analysis of the total score	cy ch Length DB	4 4 10	1 798 10 0 294 9 8 417 10 0 510 9
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602559348F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4697338 5', mRNA sequence.
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                               /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
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100.0%; Pred. No. 2.8e-142;
ive 0; Mismatches 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capbs - Femail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., P.
Emmert-Buck, M.D., Ph.D.
                                               Length
                                            Score 567; DB 10;
Pred. No. 5.1e-160;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10615 row: c column: 19
High quality sequence stop: 766.
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/lab_host="DH108 (TI phage-realstant).
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
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/lab_host="DH10B (phage resistant)"
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco.
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                                                    ttggttgttttttttgagacagagtctcactctgttgcccaggctggagtgcagtggca
                                                                                                                                          1342 gtagagacggggttttcccacgttggccgggctggtctcaaactcttgacctcaagtgaa
                                                                                                332 AACAAGGAGCCTACTTTTAGCTCCTATTCCACCTTCTCACACGTTTTTG-TGT
                                                                                                                                                                                                                                                                                  570 GTAGAGACGGGTTTTCCCACGTTGGCCGGGCTGGTCTCAAACTCTTGACCTCAAGTGAA
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/db_xref="taxon:9606"
/clone="INAGE:2375892"
/clone="INAGE:2375892"
/sac="maie"
/dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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AI880389.1 GI:5554438
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1 (bases 1 to 873)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Stausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC.

CONA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
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0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 449; Conservative (
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Briones, M.R.,

expressed

Paulo-SP,

us-09-813-492-1.oli.rst

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Br0687"
/db_xref="house."
/db_xref="house."
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
Fig. +57-11-570701
Fig. 
                    Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 ccatcgtggccttggctgtctgtgcggccctacatgcctcagaagccatacttcccattg
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF sequence tags sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/organism="Homo sapiens"
/db_xef="texon:9606"
/clone="InkdE:3838987"
/clone=lib="NIH_MGC_55"
/clone=lib="NIH_MGC_55"
/clone=lib="NIH_MGC_55"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DbH10B (Tl phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
/note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
/note="Organ: bone 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 399)
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                           found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM526 row: k column: 20
High quality sequence stop: 550.
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100.0%; Pred. No. 2.3e-103;
Live 0; Mismatches 0;
                                                                                                                      quality sequence stop: 550 Location/Qualifiers
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TGGACTTGGCCATGATT 449
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Briharia; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 57);
E Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldman, P. and Wilson, R. The Wash Mark EST Project

L Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                      N63913 577 bp mRNA linear EST 01-MAR-1996 za27h10.s1 Soares fetal liver spleen lNFLS Homo sapiens CDNA clone IMAGE:293827 3' similar to contains element MIR repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 356.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1609 gggcctccctgctggctagtcccaagcggtggtgttgccaggatgtcttggaggtgataa 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1729 ctaatatocotcattgaotatttagoatttaatttatttactttootgaoatttotgoaa 1788
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GACTTGCCCAGGTCACACAGGAAGTGGCAGAGACAAGCTTTTTAAATAAGAAAAATTAA
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100.0%; Pred. No. 6.6e-77;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:293827"
                                     ;, mRNA sequence.
N63913
N63913.1 GI:1211742
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Matches 289;
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
Info@tmage.llnl.gov
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Cogan: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco R1; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 132276-1333911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                             BE463561 362 bp mRNA linear EST 27-JUL-2000 hw25b05.xl NCI_CGAP_Kid11 Homo sapiens CDNA clone IMAGE:3183921 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacttgcccaggtcacacaggaagtggcagagacaagctttttaaataagaaaaattaa 1908
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100.0%; Pred. No. 3.5e-87;
tive 0; Mismatches 0;
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:3183921"
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1. .362
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Unpublished (1997)
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                                                                                                                          mRNA sequence.
BE463561
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T. R., Williamson, A., Wohlfing, T., and Wilson, R.
The Washu-Marck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop:
Location/Qualifiers
1. 437
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/db_xref="GDB:3801674"
/db_xref="taxon:9606"
/db_axref="taxon:9606"
/clone="THAGE:293877"
/clone=lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                 Length 437;
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100.0%; Pred. No. 9.8e-69;
Live 0; Mismatches 0;
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Length 472;

Score 254; DB 10;

12.6%;

Query Match

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/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                      Score 194; DB 10; Pred. No. 9e-49; O;
                      9.6%; scc. No. 100.0%; pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3874117"
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N27569.1 GI:1142050
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Matches 194; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
                                         1753 gcatttaatttatttttcctgacatttctgcaagctttgtattttatatttccacttt 1812
                                                                                                                                         1813 atagatgaggaaatttgaggetettagaggtaaaatgaettgeecaggteacaggaag 1872
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                     NHH-WGC http://mgco.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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  Pred. No. 2.2e-66;
100.0%; Pred. ...
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High quality sequence stop: 613.
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                Matches 254; Conservative
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N27569 487 bp mRNA linear EST 30-DEC-1995
yx43b10.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:264475 5', mRNA sequence.
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Contact: Wilson Ry

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Email: esfewatson.wustl.edu

High quality sequence stops: 303

Source: IMAGE Consortium, LLNL

This clone is available royalty free through LLNL: contact the Insert Length: 541 Std Error: 0.00

Seq primer: T7

High quality sequence stop: 303.

High quality sequence stop: 303.
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1 (bases 1 to 487)
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11 (laser,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trewaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 112 c 109 g 147 t 5 others
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMA52 row: g column: 23
High quality sequence stop: 729.
Location/qualifiers
I. 798
                                                                                                                                                                                                                  102 CACCATGCCGGGTCACACGTTTGAGTACCATTGTGCCATTCTTTTTGGCCTT 161
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99.6%; Pred. No. 1.4e-47;
tive 0; Mismatches 1;
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AUTHORS
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
    Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Rechnologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bi.llnl.gov/bbrpy/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 285.
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/tissue_type="moderately differentiated adenocarcinoma"
/tissue_type="moderately differentiated adenocarcinoma"
/tab_nost="bullob"
/note="Organ: colon: Vector: pCWV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot 50. Average insert size 1.3zkb.
Normalized version of NCI_CGAP_CO18. Library constructed
by Life Technologies."
38 c 40 g 132 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW083576 294 bp mRNA linear EST 14-OCT-1999 xcl8g08.xl NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2584670 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR: This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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Similarity 100.0%; Pred. No. 1e-33;
4; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2584670"
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Unpublished (1997)
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Search completed: October 7, 2002, 12:07:31 Job time: 9086 sec

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Searched:

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Database

Perfect score:

Title:

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Scoring table:

immune/haema immune/haema immune/haema immune/haema 1mmune/haema 1mmune/haema

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/transl_except= (pos: 254..256,
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AAV38293
AAZ91767
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AAS28165
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Copyright (c) 1993 - 2000
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                                                                                                                                                                                               mammary associated chemokine and related polynucleotides, useful r detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3117 BP; 860 A; 582 C; 566 G; 921 T; 188 other;
                                                                                                                Dyster LM, Frustaci JM, Papsidero LD;
                                                                                                                                                                                                                                                 Claim 19; Page 18-20; 76pp; English
                                                                                (CODO-) CODON DIAGNOSTICS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated chemokine (MACK).
                              98US-0092155.
98US-0071899.
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P-PSDB; AAY29092, AAY29093
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15; 1090 1848 1849 ttattttgtcatttagagttcataaatattagggtttattttctaaatagaatagtttaa 1908 Gaps ggtatgcaaatgtagccaataatatactcaaactcctgggctcaagcgatcctcccacct tagcctcccaaagtactgggattataggtgtgagccacagtgcctggcctaattatttc 1729 tagcctcccaaagtactgggattataggtgtgagccacagtgcctggcctaatttttc 1909 actaaatataacttcaaaacgtctagtttgagtagctaccgttgtttggattgaaattt actaaatataacttcaaaacgtctagtttgagtagctaccgttgtttggattgaaatttt 20; Length 3117; 18; Indels 92; 51.3%; Score 1035.2; DB 2 86.5%; Pred. No. 5.7e-206; 11ve 73; Mismatches 92; Best_Local Similarity 86.5 Matches 1172; Conservative Query Match Best Local S 1669 671 731 851 911 971 1031 2029

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                                                                                                                                                                                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were
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Pred. No. 1.4e-103;
1; Mismatches 4; Indels 0;
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                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                    Claim 1; Page 2980-2981; 9803pp; English.
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99.1%;
                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                            99US-0157137.
99US-0163280.
                                                                    28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 99.1
Matches 544; Conservative
                                                                                                                                                      Ruben SM, Barash SC,
                                                                                                                                                                               2001-235357/24.
                                                                                                                                                                                           P-PSDB; AAG74697
                      WO200122920-A2.
                                                                                             29-SEP-1999;
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antific Lammatory; antirheumatic; antiarthritic; immunosupressive;
w antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; eacemas;
w antiagregant; haemostatic; vulnerary; antilicer; osteopathic; eczema;
w dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
w dermatological; antidepressant; nootropic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antidiabetic; inflammation;
w miniostimulant; gene therapy; antisense therapy; vaccine; inflammation;
w miniostimulant; gene therapy; antisense therapy; vaccine; inflammation;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
w thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
w Alzebimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM99166 to AAM99904 encode the human proteins given in AAM25225 to AAM35963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antiirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; anti-HIV; fungicide; antimutagen;
                                                                                                                Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e\,.g\,. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein encoding cDNA sequence SEQ ID NO:255.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                    ctgttaagcagtggatggatggcaagctgccaagaaaaatggtaaaggaaatgtttgcc
                                                                                                                                                                                                                    cagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttcca
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                                                                                                                                                                     DB 22; Length 698;
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                                                                                                                                             Sequence 698 BP; 172 A; 170 C; 188 G; 168 T; 0 other;
                                                                                                                                                                    24.9%; Score 501.8; DB 22; 99.6%; Pred. No. 3.5e-95; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 caagtggacttggccatgattggtt 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human C-C chemokine DVic-1 cDNA.
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Best Local Similarity 99.69
Matches 503; Conservative
                                                                                                                            neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV38291;
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This cDNA sequence codes for human DNAX Vic-1 (DVic-1) (see AAW60649),
a novel C-C chemokine. DVic-1 cDNA can be obtained from e.g. skin,
epithelial or wound healing libraries by PCR amplification or by
cepithelial or wound healing libraries by PCR amplification or by
cepithelial or wound healing libraries by PCR amplification or by
charles and are probably ESTS from a similar transcript. These show
chomology and are probably ESTS from a similar transcript. The
chemokine motifs of these 2 ESTS were compared, and a consensus
sequence was derived and confirmed as encoding Dvic-1. The Dvic-1
gene has been localised to human chromosome 9p13. An alternative
chomokine properties of these AAV88296 for human Dvic-1 is also disclosed.
Also claimed is novel human DNAX Groin Wound expressed CC chemokine
(DGWCC) (See AAW60649), as well as expression vectors and host cells.
Dvic-1 and DGWCC play a role in the regulation or development of
neuronal or haematopoletic cells, e.g. lymphoid cells, which affect
immunological responses. They can be used in the treatment of
conditions associated with abnormal physiology or development,
including abnormal proliferation, e.g. cancerous conditions or
degeneration, and atrophy may be modulated by appropriate
the requestion and atrophy may be modulated by appropriate
the requestion.
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100.0%; Pred. No. 2.2e-94;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         Vicari A, Zlotnik A;
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                                             Location/Qualifiers
                                                                                                                                                                                                                                                                         96US-0761071
96US-0031805
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56..121
/*tag= b
122..436
/*tag= c
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                                                            56..439
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P-PSDB; AAW60649.
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tacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaaggctcc<sup>.</sup>182
                                                                                                                                               Morales
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              tggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttggctgctg
                                                                                   ataaaactccttattagagagtctacagataaatctacagagacaattcctcaagtggac
                                                                           agtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccacaggaaga
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                              tggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttggctgctg
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Zlotnik A;
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1..1089
                                                                                                                                                                                                                                                                      Primate Vic nucleotide sequence.
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56..121
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122..436
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99US-0322580.
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Kellermann S, McEvoy
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DB; AAB01450.
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                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                 AAA47545
                                                                                                                                                                                                           RESULT
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Human; G-protein coupled receptor; GPR27; antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian; cardiant; hypertensive; hypotensive; diuretic; osteopathic; antiulicer; cerebroprotective; antialler; antiemetic; tranquilliser; nootropic; antidepressant; neuroleptic; anticonvulsant; vaccine; gene therapy; infection; pain; cancer; diabetes; obesity; anorexia; bulimia, asthma; Parkinson's disease; acute heart failure; hypotension; hypertension;
                                             Modulating movement of a cell within or to the skin of a mammal can be achieved by administering an antegonist or agonist of cutaneous T cell-attracting chemokine (CTACK) or vasoactive intestinal contractor (Vic) chemokine. The antegonist is selected from a mutein of natural CTACK or Vic, an antibody which neutralises CTACK or Vic or an antibody which plock GPRZ ligand binding. The CTACK or Vic agonists or antagonists are useful for treating medical conditions or diseases associated with immunological conditions of the skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agagagactcgccatcgtggccttggctgtctgtgcggccctacatgcctcagaagcca 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agtggatgaaagtgcaagctgccaagaaaatggtaaaggaaatgtttgccacaggaaga 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agagaggactcgccatcgtggccttggctgtctgtgcggcctacatgcctcagaagcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacatacggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                   Sequence 731 BP; 206 A; 193 C; 163 G; 168 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                Score 498; DB 21;
Pred. No. 2.2e-94;
0; Mismatches 0;
Page 68-69; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                            24.7%; Sc.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573 ttggccatgattggttgt 590
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17-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
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AAA52456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic disorder; neurological disorder; dyskinesia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocalisation studies, as tools for tissue expression studies, or as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G-protein coupled receptor GPR27 polypeptides and polynucleotiduseful as vaccines or for treating diseases, e.g. infections, pain, cancers, urinary retention, osteoporosis, stroke, psychotic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic reagent for detecting mutations in the associated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agagaagtectegeceategtggcettggetgtetgtgeggeeetaeatgeeteagaageea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 778 BP; 245 A; 194 C; 168 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 29; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0361564.
                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000WO-US19855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 498; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testa TT, Vawter L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-191359/19.
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                                                                                                                                                                                                             WO200107482-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-1999;
                                                                                                                                                                                                                                                                                 01-FEB-2001
                                                                                                                                               Homo
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Human GFRP-2; growth factor related molecule; breast tissue;
breast tumour; CC chemokine; hTECK homologue; developmental disorder;
cell proliferative disorder; immune disorder; reproductive disorder;
cardiovascular disorder; bacterial infection; viral; fungal; parasitic;
cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis;
consensus; ss.
                                                                                             512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treatment of disorders associated with its activity including developmental, cell proliferative, immune, reproductive and cardiovascular disorders and infections
                                                                                                agtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccacaggaaga 369
                                                                                                                                              572
                                                                                                                                                           ataaaactccttattagagagtctacagataaatctacagagacaattcctcaagtggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents cDNA encoding human growth factor related molecule GFRP-2. cDNA encoding GFRP-1 was initially identified in breast tissue cDNA library, and the present sequence represents a
                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human growth factor related molecule GFRP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Human GFRP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 74; 80pp; English.
                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0181711.
98US-0209547.
99US-0313457.
                                                                                                                                                                                                                                                                               AAA52456 standard; cDNA; 566
                                                                                                                                                                                               573 ttggccatgattggttgt 590
                                                                                                                                                                                                            99WO-US25458
                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350695/30.
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                                                                                                                                                                                                                                                                                                                                25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1998;
11-DEC-1998;
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Homo sapiens.

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consensus derived from several overlapping and/or extended cDNA clones. GFRP-2 is probably a CC chemokine and has chemical and structural homology with hTECK (20% identity). GFRP-1 and hTECK are both basic proteins, having isoelectric points of 10.1 and hTECK are both basic and nortumorous breast tissue. GFRP proteins (AAB0300-B0303), nucleotides encoding them (AAA5245-A5548), GFRP agonists and antagonists may be used to treat a wide variety of diseases associated with increased or decreased expression or activity of GFRP proteins. Conditions which may be treated include developmental disorders, cell proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., menstrual cycle disorders) cardiovascular disorders (e.g., arteriosclerosis) and bacterial, viral, fungal or parastitc infections. Additionally, GFRP proteins and nucleotides can be used in the diagnosis of such disorders.
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                                                                                                                                                                                                                                                                                                                                                               togaacagcetcaettgtgttgetgtcagtgccagtagggcaggcaggaatgcagcagag 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396
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                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccacaggaagaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccatggcaagaggacagtaacagggcacatcaggggaaacacgaaacatacggccataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                                                                    Length 566;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                       Sequence 566 BP; 152 A; 137 C; 144 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #12362.
                                                                                                                                                                                                                                                                                                  Score 441; DB 21; Pred. No. 1.5e-82; 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS76558 standard; cDNA; 675
                                                                                                                                                                                                                                                                                                  Match 21.9%;
Local Similarity 96.0%;
les 485; Conservative
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                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
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polymerase chain reaction (FRS) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (FRS) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat diseases states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequences and for this patent did not appear in the printed converting the printed converting the printed converting the convertion of the printed converting the converting converting the converting converting the converting c
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Pred. No. 1.2e-81;
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                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #17066
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23-AUG-2000; 2000US-0649167.
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forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemocactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds
diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                    Score 409.8; DB 23; Length
Pred. No. 4.4e-76;
0; Mismatches 7; Indels
                                                                                               Sequence 474 BP; 134 A; 112 C; 124 G; 104 T; 0 other;
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97.3%;
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Matches 460;
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Homo sapiens
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                                                                                                                            human secreted proteins, and encode the proteins given in AAY1531 to human secreted proteins, and encode the proteins given in AAY11533 to human secreted proteins, and encode the proteins given in AAY11533 to AAY11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for disponsals and therapy. The proteins obtained may have cytokine activity, call proteins obtained may have cytokine activity, call proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, receptor/ ligand activity, haemostatic and thromolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity on other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a cell.
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                                                                New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from liver, lung, large intestine, colon, thyroid and pancreas tissue
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100.0%; Pred. No. 2.5e-70;
iive 0; Mismatches 0;
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                                                                                                           Claim 1; Page 276-277; 398pp; English.
           Dumas Milne Edwards J,
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Best Local Similarity 100.
Matches 382; Conservative
                               WPI; 1999-153700/13.
                                            P-PSDB; AAY11658
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                                                                vaccine; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Xaa = unknown; the start and stop codons
                                               Chemokine; breast tissue; breast milk; breast disease; vaccine; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; ss.
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Human mammary associated chemokine (MACK) open reading frame.
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                                                                                                                                                                                                                                                                                                                                                      /codon_start= 3
/transl_except= (pos: 207..209, aa: Xaa)
/transl_except= (pos: 270..272, aa: Xaa)
/product= "MACK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 381 BP; 110 A; 91 C; 97 G; 81 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are not indicated"
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                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 20; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start= 3
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69..378
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Best Local Similarity 99.5
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          386
                                                                                                                                                        ggaagaaacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacat 506
                                                                                                                                                                  DVic-1; DNAX Vic-1; C-C chemokine; cytokine; human; immune system; cancer; cell proliferation; therapy; diagnosis; HHFFQ25R; ss.
                                               aagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaa
                                      ggctcctggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttgg
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                                                                                                                                                                                                                                                                                                                          Human C-C chemokine DVic-1 EST HHFFQ25R
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                                                                                                                                                                                                                 acggccataaaactccttatt 381
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treating abnormal physiology
degenerative conditions
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96US-0031805.
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Chemokine; breast tissue; breast milk; breast disease; vaccine; human; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; probe; ss.
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including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. Abnormal proliferation, regeneration, degeneration, and atrophy may be modulated by appropriate therapeutic treatment using products of the invention. The procan also be used for detection, diagnosis and drug screening.
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                                                                                                                                                                                                                                                                                                                                                                 Score 369.6; DB 19;
Pred. No. 1e-67;
0; Mismatches 70;
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cancer; cell proliferation; therapy; diagnosis; HOEDH11R;
                                                                                                                                                                                                                                                                                                WPI; 1998-322730/28.
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                                      Homo sapiens
                                                                     WO9823750-A2
                                                                                                                                        26-NOV-1997;
                                                                                                                                                                         05-DEC-1996;
                                                                                                                                                                                                                                                               Hedrick JA,
                                                                                                                                                                                          27-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgctgtcatccttcatgtcaagcgcagaagaatctgtgtcagcccgcacaaccatactgt 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammary associated chemokine and related polynucleotides, useful or detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVic-1; DNAX Vic-1; C-C chemokine; cytokine; human; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                           The invention provides an isolated human chemokine, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human mammary associated chemokine (MACK) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 302; DB 20;
Pred. No. 1.1e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 311 BP; 65 A; 77 C; 72 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human C-C chemokine DVic-1 EST HOEDH11R,
                                                                                   Frustaci JM, Papsidero LD;
                                                                                                                                                                                                      Claim 29; Page 26; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                   DIAGNOSTICS LLC.
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Best Local Similarity 99.3%;
Matches 302; Conservative
98US-0092155.
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09-JUL-1998;
              20-JAN-1998;
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                                                                                   Dyster LM,
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This sequence defines EST HOEDHIIR obtained from a human osteoblast
library. It shows high homology to EST HHFFQ2FR (see AAV38292)
cobtained from a human footal heart library. The two ESTs are
probably from a similar transcript. The chemokine motifs of the
two ESTs were compared, and a consensus sequence was derived and
subsequently confirmed as encoding human DNAX vic-1 (DVic-1) (see
AAW60649), a novel C-C chemokine. CDNA (see AAV38291) encoding Dvic-1
can be obtained from e.g. skin, epithelial or wound healing
libraries. DVic-1 plays a role in the regulation or development of
neuronal or haematopoietic cells, e.g. lymphoid cells, which affect
conditions associated with abnormal physiology or development,
including abnormal proliferation, e.g. cancerous conditions or
degenerative conditions. Abnormal proliferation, regeneration,
degeneration, and atrophy may be modulated by appropriate
therapeutic treatment using products of the invention. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 cctcagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatt 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccagaaggctcctggnaaagagtgaatatgtgtcgcatccagagagctgatggggattgt 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                              treating abnormal physiology or development, e.g. cancerous or degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacttggctgctgtcatccttcatgtcaagcgcagaagaatctgtg-tcagcccgcacaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can also be used for detection, diagnosis and drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 445 BP; 123 A; 112 C; 108 G; 95 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 261.4; DB 1
88.8%; Pred. No. 3.2e-45;
                                                                                                                                                                                                                 Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 61-62; 71pp; English.
                                                                                                                                                                                                                 Vicari A,
97WO-US21092
                                                         96US-0761071
96US-0031805
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                                                                                                                                                                                                                 Morales J,
                                                                                                                                                       (SCHE ) SCHERING CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, imaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 gagigaataigigicgcalccagaggigatggggattigigacttggctgctgtcalcc 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                  Human; breast specific gene; breast specific marker; BSG; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.2%; Score 246; DB 21; Length 253; Best Local Similarity 97.2%; Pred. No. 4.5e-42; Matches 246; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 253 BP; 52 A; 64 C; 70 G; 60 T; 7 other;
                                                                                                                                                                        Human breast specific gene LS clone 2299454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 41; 45pp; English.
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                                                                                         AAZ91767 standard; DNA; 253 BP.
                                                                                                                                                                                                                                                                                                                                                                                                  Cafferkey
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                                                                                                                                              01-JUN-2000 (first entry)
                                                                                                                                                                                                                breast cancer; therapy; ss
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558 attcc 562
                        437 ttccc 441
                                                                                                                                                                                                                                                                  WO200008210-A1
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                     22-JUL-1999;
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                                                                                                                     AAZ91767;
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em_estin: *
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em_estol: *
em_estol: * gb_est1:*
gb_est2:*
gb_htc:* em_estba:* *:ssb_dp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	BG682175 602629474	BF034600 601455024	N63913 za27h10.s1	AW469978 xr27a11.x	BG530240 602559348	BG532385 602561892	AI880389 at55a07.x	BG614513 602642663	BE748488 601571978	N98285 za27h10.rl	BE088415 CM0-BT068	N20300 yx43b10.s1	BE463561 hw25b05.x	AZ575795 AST-T29B0	BE004848 MR2-BN011	N27569 yx43b10.rl	BB617469 BB617469
QI.	BG682175	DF034600	N63913	AW469978) BG530240	DG532385	AI880389) BG614513	DE748488	N98285	BE088415	N20300	BE463561	AZ575795	BE004848	N27569	BB617469
å Query Match Length DB	816 10	698 10	577 10	508 9	869 10	798 10	450 9	1066 10	873 10	437 10	399 9	472 10	362 10	345 12	510 9	487 10	695 9
Query Match	36.4	31.6	26.3	25.2	24.7	22.5	22.2	21.5	20.8	19.3	18.7	17.9	17.9	14.9	14.5	14.1	14.0
Score	734.2	638.2	530.2	208	497.8	454.2	448.4	434	418.6	389.2	377.2	361.8	360.4	301	292.6	283.4	281.8
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/clone_lib="NIH_MGC_66"
//tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="NOGAn: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
            Euteleostom1;
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                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can intp://image.llnl.gov
http://image.llnl.gov
Plate: LLAMS591 row: o column: 05
High quality sequence stop: 698.
Location/Qualifiers
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            Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                     (bases 1 to 698)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection
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                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3859036"
                                                                                            Contact: Robert Strausberg, Ph.D.
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                       Length 816;
                                                                  Indels
                                       10;
                                       Score 734.2; DB 10
Pred. No. 1.9e-99;
); Mismatches 3;
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                                       36.4%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 508)

NoT-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (GGAP),

Tumor Gene Index

In Opublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Email: cgapbs-rémail.nih.gov

Ensert-Buck, M.D., Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW469978 508 bp mRNA linear EST 24-FEB-2000 xz27all.xl NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761340 3',
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                                                                                                                                                                                                                                                           1566 ccaatagagagcaggagccactttatcaggtggcaggtgtcccgggcctccctgctggct 1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1746 ctatttagcatttaatttattttcctgacatttctgcaagctttgtatttatattt 1805
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                                    572 TTTTGNATTTTTAGTAGAGACGGGTTTTCCCCACGTTGGCCGGGCTGGTCTCAAACTCTT
                                                                                                                                                                                      tttttgtccatagaggcttcaagatagataggtaagagcccagtagtgttcataagaag-
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Location/Qualifiers 1..508
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldman, P. and Wilson, R.

The Washu-Merck EST Project

L Unpublished (1995)

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Washington University School of Medicine
4444 Forest Park Park Park Way, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Fmail: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                              N63913 577 bp mRNA linear EST 01-MAR-1996 za27h10.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:293827 3' similar to contains element MIR repetitive element
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: m13 -40 forward High quality sequence stop: 356.
               1329 ttttgtatttttagtagagacggggttttcccacgttggccgggctggtctcaaactct 1388
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Pred. No. 3.1e-69;
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/organism="Homo sapiens"
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ilarity 98.8%;
Conservative
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N63913
N63913.1 GI:1211742
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL

COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION

N63913/c

Best Local

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BASE COUNT

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261
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602559348F1 NIH_MGC_61 Homo sapiens cDNA clone IMACE:4697338 5',
MRNA sequence.
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                                          /lab_host="DH10B"
/note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sall;
/note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
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                                                                                                                                                                                                                                     ttcataagaagccaatagagagcaggagccactttatcaggtggcaggtgtcccgggcct 1614
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/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade,
pooled_tumors"
                                                                                                                                                                                                                                                 TATTTATATTTCCACTTTATAGATGAGGAAATTTGAGGCTCTTAGAGGTAAAATGACTTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Length 508;
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Best Local Similarity 100.0%; Pred. No. 6.2e-66;
Matches 508; Conservative 0; Mismatches 0;
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/lab_host="mbtyonal trapped resistant,"
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/note="Organ: testis: Vector: pDNR-LIB (Clontech); Site_1:
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/note="Organ: testis: Site_2: Site_2: Site_2: Sil (gpccattaggcc);
/note="Organ: testis: Site_2: Site
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1525 row: p column: 11
High quality sequence stop: 748.
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Pred. No. 1.6e-64;
0; Mismatches 2; Indels
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    869
/organism="Homo sapiens"
/db_xref="taxon:9606"

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Matches 499; Conservative
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AI880389 450 bp mRNA linear EST 23-AUG-1999 at55a07.xl Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2375892 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Glbco.
Location/Qualifiers
                                                                                         619
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Pred. No. 4.2e-57;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="IMAGE:2375892"
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Best Local Similarity 99.8
Matches 449; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Exammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RAL Onpublished (1999)

Contact: Robert Streausberg, Ph.D.
Contact: Robert Streausperged by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.lln.ipgov.
Clone distribution: MGC clone distribution information can be http://image.lln.ipgov.
Plate: LLCM153 row: 9 column: 23

High quality sequence stop: 729.
Flate: LLCM153 row: 9 column: 23

High quality sequence stop: 729.
Colone-lib* NHL MGC.G.
Clone-lib* NHL MGC.G.
Clone-lib* NHL MGC.G.
Clone-lib* NHL MGC.G.
Contained cDNA was prepared from cell line RNA.
Colone-lib* Standard CDNA was prepared from cell line RNA.
Colone-lib* Standard CDNA was prepared from cell line RNA.
Colone-lib* Standard CDNA was constraoused of colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clonectined Library.
Colonel Librar
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                                                                                         BG532385 1793-APR-2001 002561892F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699822 5',
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Pred. No. 4.6e-58;
0; Mismatches 8; Indels
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Best Local Similarity 97.8%;
Matches 492; Conservative
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                            RESULT
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BE748488 873 bp mRNA linear EST 15-SEP-2000 601571978F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838987 5',
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGGCGGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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I (bases 1 to 873)

NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                      Length 1066;
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Pred. No. 3.9e-55;
0; Mismatches 20;
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95.1%;
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/lab_host="DH10B (T1 phage-resistant)"
/note="Corgan: testis; Vector: pDNR-LiB (Clontech); Site_1:
Sfil (ggcgcctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG614513 1066 bp mRNA linear EST 18-APR-2001 602642663F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773711 5', mRNA sequence.
BG614513.1 GI:13665884
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                                                                                                                                                                                                   tgcccaggtcacacaggaagtggcagagacaagctttttaaataagaaaaattaataaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4773711"
/clone_lib="NIH_MGC_61"
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/organism="Homo sapiens"
/db_xref='taxon.9606"
/clone='InAce:3838987"
/clone='InAce:3838987"
/clone='InAce:25"
/tissue_type="from acute myelogenous leukemia"
/lab_host="blu108 (TI phage-resistant)
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); plouble-stranded cDNR was prepared from cell line RNA.
); Double-stranded cDNR was prepared from cell line RNA.
); adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCAGCATG-dT(30)BN 3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by clontech
Laboratories (Palo Alto, CA)."
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              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. k column: 20
High quality sequence stop: 550.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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Pred. No. 8.1e-53;
0; Mismatches 14
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Best Local Similarity 95.8%;
Matches 474; Conservative
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10

RESULT N98285

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l. 437
/organism="Homo sapiens"
/db_xref="Chois:3801674"
/db_xref="Chois:3801674"
/db_xref="Chois:3801674"
/db_xref="Chois:3801674"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/dev_stage="20 week-post conception fetus"
/dev_stage="20 wee
N98285 437 bp mRNA linear EST 10-APR-1996 za27h10.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:293827 5' similar to contains Alu repetitive element; , mRNA
                                                                                                                                                                                                                                                                      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 437)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
                                                                                                                                                                         N98285.1 GI:1269708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I bases 1 to 472)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulthman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldamn, P. and Wilson, R.

R, Williamson, A., Wohldamn, P. and Wilson, R.

R, Williamson, A., Wohldamn, P. and Wilson, R.

Gontact: Wilson RK
Mashington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N20300 472 bp mRNA linear EST 18-DEC-1995 yx43bl0.sl Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264475 3', mRNA sequence.
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lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT713D (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
261
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                                                                                                                                                                                                                                                                     262 cagaaggetectggaaagagtgaatatgtgtegeatecagagagetgatggggattgtga 321
                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                 202 ctcagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttc
                                                                                                                                                                                                        1. 472
/organism="Homo sapiens"
/db_xref="GDB:3874117"
/db_xref="taxon:9606"
/clone="IMAGE:264475"
/clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 CCACAGGAAGAACACCCATGGCAAGAGGAACAGTAACA 399
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Location/Qualifiers
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N20300.1 GI:1125255
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="BT0667"
/dclone_lib="BT0667"
/dclone_lib="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 399)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=CMO-BT0687-210
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stope: 399.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                            241 TGCTGGAATTACCAGCGTGAG-CACCATGCCGGGCTCACACGTTTGAGTTGATACCATTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                             399 bp mRNA linear CMO-BT0687-210300-297-f08 BT0687 Homo sapiens cDNA, BE088415.1 GI:8478815
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Email: capabs.remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
infowing the I.M.A.G.E. Consortium/LLNL, send email to:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 362)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Oppublished (1997)
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Pred. No. 2.6e-44;
0; Mismatches 2; Indels
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nes 374; Conservative
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a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purlification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatina Bonaldo.
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AZ575795.1 GI:11562106
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1 (bases I to 345)
1 (bases I to 345)
4 (bases I to 345)
7 Durick, K. and Pollok, B. Exon-trap tags from a f47D GenomeScreen(TM) Library Unpublished (2000)
Contact: Greg Henkel
Gene Expression
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                          1. 362
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                          /clone="IMAGE:3183921"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatima Bonaldo.
81 c 6
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1. 510
/organism="Homo saplens"
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/dev_stage="Adu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MR2-BN0114-020 S00-013-bl2&t3-2000-05-02&t4-1) Seq primer: puc 18 forward High quality sequence start: 21 High quality sequence start: 21 High quality sequence stop: 442.
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira.P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 4.3e-34;
0; Mismatches 19
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                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A.
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Local Similarity 94.1%;
nes 304; Conservative
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 bp mRNA linear EST 05-JUN-200. BE004848 GI:8255081
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/db_xref="taxon:9606"
/clone_lib="cenetrap T47D Human Breast Carcinoma Library"
/tissue_type="Carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        total
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/cell_type="fpithelial"
/cell_line="T47D"
/note="Organ: Breast; Vector: pAmp-1; 3' RACE of from genetrap pools; shotgun clone in pAmp-1 and transform DH5-alpha competent bacteria."
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Pred. No. 2.9e-35;
); Mismatches 0;
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APPLICANT: Papaidero, Lawrence D
APPLICANT: Dyster, Lyn M
APPLICANT: Frustaci, Jana M
TILLE REPRENCE: 200755/1002
FILE REPRENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLER APPLICATION NUMBER: 60/071,889
EARLER FILING DATE: 1998-01-20
EARLER APPLICATION NUMBER: 60/092,155
EARLER PILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.3%; Score 1035.2; DB 4; Length
86.5%; Pred. No. 2.6e-222;
.ive 73; Mismatches 92; Indels
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              US-08-658-136-1

US-09-301-65-3

US-09-301-65-3

US-08-370-975B-6

US-08-370-975B-1

US-08-319-975B-1

US-08-313-817-3

US-08-313-817-3

US-08-313-817-3

US-08-484-257-20

US-08-484-257-20

US-08-99-927-5

US-08-99-927-5

US-08-661-819-5

PCT-US95-01829-5

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US-08-99-165-5
                                                                                                                                                                                                                                                                                          US-09-009-656-11
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09146580A Patent No. 6306653 GENERAL INFORMATION:
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 NAME/KEY: unsure
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Matches 1172;
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-146-580-7
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US-08-146-580-11
US-09-101-702-1
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PCT-US95-07201-43
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US-08-488-020
US-08-483-553-20
US-08-488-011B-20
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                                                         Sequence 7, Application US/09146580A
| Sequence 7, Application US/09146580A
| Patent No. 6306653
| GENERAL INFORMATION:
| APPLICANT: Papsidero, Lawrence D
| APPLICANT: Papsidero, Lawrence D
| APPLICANT: Frustaci, Jana M
| TILLO OF INVENTION: DEFECTION AND TREATMENT OF FILE REFERENCE: 200755/1002
| CURRENT APPLICATION NUMBER: US/09/146,580A
| CURRENT FILING DATE: 1998-09-03
| EARLIER FILING DATE: 1998-01-20
| EARLIER FILING DATE: 1998-01-20
| EARLIER FILING DATE: 1998-01-09
| SALIER FILING DATE: 1998-07-09
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: Patentin Ver: 2.0
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US-09-146-580-11/c
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Best Local Simi
Matches 379;
                                           RESULT 2
US-09-146-580-7
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OD: experimental /function= "(translation start:
                                                                                                        CIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOMBER: US/08/814,095
FILING DATE:
CLASSIFICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION NUMBER: 38,972
RECISTRATION NUMBER: 38,972
RECISTRATION NUMBER: 2391.00066
TELEPOMONICATION INFORMATION:
TELEPOMONICATION INFORMATION INFORM
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OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
FEATURE:
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LOCATION: 24090..25177
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: Z4110)
OTHER INFORMATION: Z5524..26009
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: Z5524..26009
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: Z4016nce= EXPERIMENTAL
OTHER INFORMATION: Z4016nce= EXPERIMENTAL
OTHER INFORMATION: Z4016nce= Z4016nc
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LOCATION: 22465..2537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
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DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
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IDENTIFICATION METHOD: experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: exon
NAME/KEY: 27255..28007
CITY: Farmington Hills
STATE: Michigan
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                     GENERAL INFORMATION:
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Pustacat, Lyn M
APPLICANT: Futsacat, Jana M
TILLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: 05/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VOY: 2.0
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: N at position 101 is either A,
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Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: (101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (162)
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LENGTH: 311
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us-09-813-492-1.rni

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complement (34528..34895)
WATION: /function= "arsenite resistance
/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 5
                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OCHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene="AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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/number= 1
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NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
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                                                                                                                        terminator
             OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
FEATURE:
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8199 GGGGTCTTGCTATGTTGCCCAGGCTGGTCTCGAACTCGTGAGCTCAAGCAATCTGCCCGC 8140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7843 TACGTATTGTGTGATCTCAGTCCTATGAGATTGGATGTTCTGCCTACACCCCAGGACCCTA 7784
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NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FEATURE:
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NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
US-08-814-095-7
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LOCATION: complement (30187..30274)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number=14
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
                                                                                                      NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 13
FEATURE:
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LOCATION: comp
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LOCATION: (4361)...(4507)
NAME/KEY: CDS
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US-09-167-681-45
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                                                                                             tttttgtatttttagtagagacgggttttcccacgttggccgggctggtctcaaactct 1387
                                                                 7544 TTTTGTAATTTTAGTAGAGGTTTCACCATGTGGGCCAGGCTGGTCTTGAATTCC 7485
                                                                                                                                                      accatgocgggctcacacgtttgagttgataccattgtgccattcctctttggcctctt 1507
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Xiaodong
APPLICANT: Liu, Xuessong
TITLE OF INVENTION: DAA FRAGMENTATION FACTOR INVOLVED IN
TITLE OF INVENTION: APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,702
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 218.2; DB 4;
Pred. No. 6.1e-40;
0; Mismatches 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMILLIAN, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512,418-3000
TELEPHONE: (512)474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09061702
Patent No. 6165737
GENERAL INFORMATION:
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58.0%;
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Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houston
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US-09-061-702-1
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1660 TGTGAGTACCTGGTCATACGGGTCAGGATAAGAATTGTCTCTGGGCTGAGGAATTC 1719
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                                                                                                                                                                                                                                                      1720 TTCTGTTCTCTGGTTTCACCAGCGTTTGGTTTGCTCATGTAATGTGGTCACCATACTCAA 1779
                                                                                                                                                                                                                                                                                                                        968 tttctgatactgaaaagaacaaaagcctgcctttctgcccagaaccttttgcctccccc 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028 agtcagttcttggagcagcactagttaggggcccagagttcggccttctgtgtggtgatt 1087
                                                                                                                                                                                           taaactaaatataacttcaaaacgtctagtttgagtagctaccgttgtttggattgaaat 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1144 acacgtt-tttgttgttgtttgtttgttttttttttgagacagagtctcactctgttgccc
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                                                                    849 acttattttgtcat-ttagagttcataaatattagggtttattttctaaatagaatagtt
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APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
TITLE OF INVENTION: SULFOTRANSPERASE SEQUENCE VARIANTS
FILE REFRENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 45
LENGTH: 8447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 45, Application US/09167681A; Patent No. 6265561; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1443 gagccaccatgccgggc 1459
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                                                                                                   631;
                                                                                                      Length
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Pred. No. 7e-39;
0; Mismatches 83;
                                                                                                   Score 216.4; DB 4;
Pred. No. 1e-39;
                                                                                                                                                  51;
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Destree
TILE AND Cancilla, Michael R.
FILE REFERENCE: Davies Col
GURENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1988-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                     0; Mismatches
     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09078294 Patent No. 6265211 GENERAL INFORMATION:
     - A, T, C or
                                                                                                   10.7%;
83.2%;
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Best Local Similarity 76.9%;
Matches 286; Conservative
                                                                                                                                                        Conservative
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US-09-078-294-9
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; OTHER INFORMATION: n
US-09-385-982-354
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                                                                                                                             Similarity
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                                                                                                                                                     Matches 258;
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US-09-078-294-9
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                                                                                                   Query Match
Best Local S
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GENERAL INCORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: 09/328,111
EARLIER PILING DATE: 1999-06-30
EARLIER PILING DATE: 1999-06-08
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-06-30
EARLIER PILING DATE: 1999-01-27
SARIER PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                                                         85; Indels
                                                                                                                                                                                                                                                                                                                                                       Score 217; DB 4;
Pred. No. 1.5e-39;
0; Mismatches 85
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Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                     Query Match 10.8%;
Best Local Similarity 76.4%;
Matches 279; Conservative
                                            LOCATION: (4827)...(4925)
NAME/KEY: CDS
LOCATION: (6322)...(6447)
NAME/KEY: CDS
LOCATION: (6543)...(6638)
NAME/KEY: CDS
LOCATION: (7137)...(7316)
NAME/KEY: CDS
                               (4827)...(4925)
CDS
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LOCATION: (1)...(631)
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LENGTH: 631
  LOCATION:
NAME/KEY:
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APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                  42060 CTCCTGACCTCAAGTGATCTGCCTCGCCTCGGCCTGAAGTGCTGGGATTACAGGCGTG 42001
42179 ATTCTCCTGCCTCAGCCTCCTGAATAGCTGGGATTACAGGCACCCA-ACACCACGCCCAG 42121
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.5%; Score 212.2; DB 5; 73.3%; Pred. No. 9.6e-39; Live 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IPM PC PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             Sequence 80, Application PC/TUS9306251
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGGALIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECHONE: 516-742-4343
TELEPHONE: 516-742-4343
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: ALLERY ALLERY S.
TYPE: ALLERY S.
TYPE: ALLERY S.
TYPE: ALLERY S.
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; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-80
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PCT-US93-06251-80/c
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                                                                                                                                             1337 gigatocgcottgcotcagcottcccaaagtgctgggattacaggtgtgagccaccatgccc 1396
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                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oblima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39 3317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 63-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
                                                                                                                                                                                                                  1457 ggctcacacgtt 1468
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CITY: Seattle
STATE: Washington
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US-08-781-891-79
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                                                                                                        1397
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1293 gatattacaggcgcccagccaccaccccgctgatttttgtattttagtagacggg 1352
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679 CACTGCAACCTCTGTCTCCTGGGTTCAAACGATTCTCCTGCCTCAGCCTCCCAAATAGCT 620
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OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMANT EPITHELIUM
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                1473 ttgataccattgtgccattcctctttgg 1501
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30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: FILPPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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; Sequence 81, Application PC/TUS9306251
; Sequence 81, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; TITLE OF ENGRENCES: 93
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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                                                                                                                                                                            1413 tgcctcccaaagtgctggaattaccagcgtgagccaccatgccgggctcacacgtttgag 1472
                                                                                             1353 gttttcccacgttggccgggctggtctcaaactcttgacctcaagtgaaccacccgcctg 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURIENT APPLICATION DATA:
FILLING DATE: 19930630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 212.2; DB 5;
Pred. No. 9.6e-39;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: NY COUNTRY: USA
                                                                                                                                                                                                                                                               1473 ttgataccattgtgccattcctctttgg 1501
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Did1gilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELER: 23 901 SANS UR
INFORMATION FOR SEQ ID NO: 81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.5%;
Best Local Similarity 73.3%;
Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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; MOLECULE TYPE:
PCT-US93-06251-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 11530
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1151 tttgttgttgtttggttgttttttttttgagacagagtctcactctgttgcccaggctgga 1210
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                                                                                                                                                                                                                                                                   full length genomic
sequence for PEDF plus flanking sequences
                                                                                                                                                                                                                                                                                                                                                                             Length 22481;
                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Munioe, David J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 212.2; DB 5;
82.5%; Pred. No. 2.4e-38;
Live 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 02210
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US-08-133-629-8/c
; Sequence 8, Application US/08133629
; Patent No. 5597694
                 TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
                                                                                                                                            TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 82.5
Matches 255; Conservative
                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: fu
OTHER INFORMATION: Se
                                                                                                                           Double
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Gree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
                                                                                                   TYPE: Nucleic Acid
STRANDEDNESS: Doub
                                                                                                                                                                                                         NAME/KEY: P1-147
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  TELEPHONE:
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Best Local S
                                                                                                                                                                                       FEATURE
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                                                                                                                                                                    tgeetcageeteccaagtaactgatattacaggegeecageeaceacecegetgattt 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9740 CCTCAGGTGATCTACCCGCCTCGGCCTCTAAAGTGCTGGGATTACAGGTTTGAGCCACT 9799
                                                                                                       Gaps
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Sequence 43, Application PC/TUS9507201

GENERAL INFORMATION:

APPLICANT: Chader, Gerald J.; Becerra, Sofia

APPLICANT: Taniwak, Takayuki

TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC

TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: New York

STATE: New York
                                                                                                     1;
                                                          Length 22481;
                                                                                                     Indels
                                                            Score 212.2; DB 4;
Pred. No. 2.4e-38;
                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: NEW JOIN COUNTRY: NEW JOIN COUNTRY: NEW JOIN COUNTRY: 10154
COMPUTER READBLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/07201 FILING DATE: 06-JUN-1995
CLASSIFICATION: DATA: APPLICATION NUMBER: 08/367,841
PRIOR APPLICATION NUMBER: 08/367,841
PRIOR APPLICATION NUMBER: 08/367,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: COCOMMED ATTER APPLICATION NUMBER: 07/952,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20264126PCT
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REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                          10.5%;
82.5%;
                                                        Query Match
Best Local Similarity 82.5<sup>s</sup>
Matches 255; Conservative
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US-08-367-841A-43
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NAME/KEY:
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US-07-906-871-15
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                                                                                                                                                                                                                                                                                                                                                         1298 tacaggogoccagocacacacocogotgatttttgtattttagtagagacggggtttt 1357
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                                                                                                                                                                                                                                                                                       Length 282;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/07906871
Petent No. 5340739
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Avraham, Shalom
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THEREOF
INVENTION: THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCES: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1418 occaaatgctggaattaccagcgtgagccaccatgccgggc 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 CCCAAAGIGCTGGGATTACAGGTGTGAGCCACCACCACCAGC
                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                      Query Match 10.5%; Score 211.6; DB 1; Best Local Similarity 85.1%; Pred. No. 9.6e-39; Matches 240; Conservative 6; Mismatches 35;
           RECISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: M0828/7001
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 517-720-3500
FELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEFAX: 617-720-2441
TELEFAX: 617-720-241

TELEFAX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 Dasse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: SINGIE
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/635,544
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FILING DATE: 19920103
Greer, Helen
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STATE: DC
COUNTRY: USA
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US-08-133-629-8
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FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.28300/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEPHONE: (202)833-753
TELEPHONE: (202)833-753
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17327 base pairs
TENGTH: 17327 base pairs
TERRET NUCLEIC ACID
STRANDEDNESS: both
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Job time: 2047 sec
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Sequence Homo sapi Homo sapi

AC010465 AC025457 AC022132 AR174328 AF266504 AF110384 AF220210 AR174329

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Homo sapi Homo sapi Human DNA

AX32966 AX334850 AX3344850 AX1344850 AC008347 AC105916 AL158844 AL158844 AL031659 AC014557

Homo sapi Homo sapi

sequence

Sequence Sequence Sequence Homo sapi

Homo sapi Human DNA

Homo sapi Human DNA

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Human DNA Homo sapi Human DNA Homo sapi

AC022165 AC006001 AD000091

CH19F15314

AC004254

AC013320 AC021016 AL390776 AC004254

Human DNA Homo sapi

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Homo Homo Homo Homo

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Homo

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AC040169

Homo sapi Homo sapi

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16653.446 Million cell updates/sec
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            GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
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PRI 08-JUN-2001
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Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 bases 1 to 107819)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107819)
DOE Joint Genome Institute and Stanford Human Genome Center.
Homo sapiens chromosome 5 clone CTD-2282F8, complete sequence. AC010465.7 GI:14329074
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 107819)
DOE Joint Genome Institute.
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Unpublished
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AUTHORS
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Description

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Query Match Length DB

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SUMMARIES

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                                              Direct Submission
Submitted (08-JON-2001) DOE Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13470140.
Draft Sequence Produced by DOE Joint Genome Institute
Submitted (28-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walhut Creek, CA 94598, USA 4 (bases 1 to 107819)

DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                          www.jgi.doc.gov
Finishing Completed at Stanford Human Genome Center
Www.shgc.stanford.doc.gov
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.4.
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Pred. No. 3e-292;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Submitted (28-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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HOMO sapiens chromosome 5 clone CTD-2202K16, complete sequence.
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DOE Joint Genome Institute and Stanford Human Genome Center.
cctcaagtgaaccacccgcctgtgcctccaaagtgctggaattaccagcgtgagccacc
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Direct Submission
Submitted (09-MAR-2000) Production Sequencing Facility, 19-
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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Doe Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Direct Submission

Submitted (09-JUN-2001) DOE Joint Genome Institute, 2800 Mitchel

Drive, Walnut Creek, CA 94598, USA

On Jun 8, 2001 this sequence version replaced gi:13470150.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.spg.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;

Estimated Total Number of Errors is 0.3.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 143372)

S DOE Joint Genome Institute.

L Unpublished

L Unpublished

E 2 (bases 1 to 143372)

S DOE Joint Genome Institute.

S DOE Joint Genome Institute.

L Unpublished

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C (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Apr 20, 2001 this sequence version replaced gi:7711706.
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                                                ACO22132 143372 bp DNA linear HTG 20-HOMO sapiens chromosome 5 clone CTD-2201J22, WORKING DRAFT SECUENCE, 9 unordered pieces.
                                                                                                                                                                                      tgtccatagaggcttcaagatagataggtaagagcccagtagtgttcataagaagccaat
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Consensus quality: 136047 bases at least 030
Estimated insert size: 119000; pulse field gel estimation
Estimated insert size: 10572; sum-of-contigs estimation
Quality coverage: 7.17 in 020 bases; pulse field gel estimation
4. NOTE: This is a 'working draft' sequence. It currently
5. consists of 9 contigs. The true order of the pieces
6. Is not known and their order in this sequence record is
7. This record the contigs are represented as
8. Tuns of N. but the exact sizes of the gaps are unknown.
8. This record will be updated with the finished sequence
8. The sa soon as it is available and the accession number will
9. The preserved.
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2: contig of 2021 bp in length
3: gap of unknown length
6: gap of unknown length
6: gap of unknown length
9: contig of 7413 bp in length
9: gap of unknown length
6: contig of 12527 bp in length
6: gap of unknown length
7: gap of unknown length
7: contig of 28247 bp in length
7: gap of unknown length
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                                                            Center clone name: CITB-H1_2201J22

    11. 143372
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

Web site: http://www.jgi.doe.gov
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 768)

Pan, J., Kunkel, E.J., Gosslar, U., Lazarus, N., Langdon, P.,

Broadwell, K., Vierra, M. A., Genovess, M.C., Butcher, E.C. and Soler, D.

Cutting edge: A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial cells in mucosal tissues
J. Immunol. 165 (6), 2943-2949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA linear PRI 27-SEP-2000 epithelial chemokine mRNA, complete
--agaggcactgagtctccataggttaaaatgccaccaaaactggccttt-gcctaatat
                                                                                                                                                                                            CAGNAGGCMCTGAGTYNCNNTAGGTTNAAATGCCACCAAAACTGGCCTTTGGCCTAATAT
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Gosslar,U., Pan,J., Kunkel,E.J. and Butcher,E.C.
Direct Submission
Submitted (10-MAY-2000) Department of Pathology, Stanfo
University, 3801 Miranda Ave, Palo Alto, CA 94304, USA
Location/Qualifiers
1.768
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                                                                                                                                                                                          Length 3117;
                                                                                                                                                         others
                   linear
                                                                                                                                                                                                              Indels
                                                                                        1 (bases 1 to 3117)
Papsidero,L.D., Dyster,L.M. and Frustaci,J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 6 23-OCT-2001;
L. 3117
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9
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Pred. No. 3.7e-228;
73; Mismatches 92;
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                 3117 bp
from patent US 6306653.
                                                                                                                                             /organism="unknown"
582 c 566 g
                                            GI:17914648
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86.5%;
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                                                                                Unclassified.
                  AR174328
Sequence 6 f
AR174328
AR174328.1
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                                                              Unknown
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Matches 1172;
RESULT 4
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RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
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   Zhang,W., He,L., Yuan,Z., Wan,T. and Cao,X.
Direct Submission
Submitted (01-DEC-1998) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Blotechnolog Institute,
800 Xiangyin Roâd, Shanghai 200433, P.R.China
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100.0%; Pred. No. 2.9e-104;
tive 0; Mismatches 0;
                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
1. 1349
                                                                                                                                                                        /note="similar to TECK"
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AF220210
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                                                                                                                             /gene="CCK1"
55. .438
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RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1349)
Zhang,W., He,L., Yuan,Z., Wan,T. and Cao,X.
A novel CC chemokine homology with TECK
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                                                                                                                                                                                                          Length 768;
                                                                                                                                                                                                          24.6%; Score 497; DB 9; Le
ilarity 100.0%; Pred. No. 2.8e-104;
Conservative 0; Mismatches 0;
/organism="Homo sapiens"
/db_xref="taxon:9606"
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53. .436
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TGGCCATGATTGGTTGT 497
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Young/P.E. Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                        others
                                                                          Tobases 1 to 381)
Papsidero, L.D., Dyster, L.M. and Frustaci, J.M. Detection and treatment of breast disease Patent: US 6306653-A 7 23-ocr-2001;
Location/Qualifiers
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Pred. No. 4e-77;
0; Mismatches
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Sequence 175 from Patent W00194629.
AX329666.1 GI:18102644
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/db_xref="taxon:9606"
                                                                                                                                                       /organism="unknown"
91 c 97 g
             GI:17914649
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Best Local Similarity 99.5%;
Matches 379; Conservative
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RVMORIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHGKRNSNRAHQGGHEYGHKTPY"
91 c 99 9 81 t
                                                                                                                                                     Soto, H., Vicari, A. and Zlotnik, A.

Soto, H., Vicari, A. and Zlotnik, A.

Direct Submission

Bibmitted (30-DEC-1999) Immunobiology, DNAX Research Institute, 901

California Ave, Palo Alto, CA 94304, USA

Location/Qualifiers
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 384)
Wang, W., Soto, H., Oldham, E.R., Buchanan, M.E., Homey, B., Catron, D., Jenkins, N., Copeland, N.G., Gilbert, D.J., Nguyen, N., Abrams, J., Kershenovich, D., Smith, K., McClanahan, T., Vicari, A.P. and
                                                                                                          gaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccaga 265
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100.0%; Pred. No. 2.8e-78;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             /product="CC chemokine CCL28"
/protein_id="AAF87205.1"
/db_xref="GI:9392591"
                                                                                                                                                                                                                                1. .384
/organism="Homo sapiens"
/organism="taxon:9606"
1. .384
/gene="SCYA28"
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Sequence 7 from patent US 6306653.
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/gene="SCYA28"
/codon_start=1
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Best Local Similarity 100.
Matches 384; Conservative
               Homo sapiens
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Papsidero, L.D., Dyster, L.M. and Frustaci, J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 11 23-OCT-2001;
Location/Qualifiers
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Pred. No. 2.1e-59;
0; Mismatches 2;
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Sequence 11 from patent US 6306653.
AR174333 GI:17914653
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77 c 72 g
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Best Local Similarity 99.3%;
Matches 302; Conservative (
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                                                                           agcggtggtgttgccaggatgtcttggaggtgataatgggacacacagaggcactgagtc 1692
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Catarrhini; Hominidae;
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Pred. No. 3.7e-73;
0; Mismatches 2;
                               Score 361.8; DB 6;
Pred. No. 3.7e-73;
0; Mismatches 2;
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AX334850
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Avalon Pharmaceuticals (US)
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/db_xref="taxon:9606"
74 c 79 g 170
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Primates;
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99.2%;
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Best Local Similarity 99.2%;
Matches 374; Conservative
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Mammalia; Eutheria;
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                                          Best_Local Similarity 99.2
Matches 374; Conservative
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1924: contig of 697 bp in 1924: contig of 678 bp in 2002; contig of 678 bp in 0122: gap of 100 bp 1012: contig of 695 bp ir
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                      ACO83975 61101 bp DNA linear HTG 08-OCT-2000 Homo sapiens chromosome 8 clone RP11-391E1 map 8, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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KEYWORDS
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COMMENT

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: gap of 100 bp
2020: contig of 714 bp in length
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820: contig of 700 bp in length
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f 702 bp in length
100 bp
f 703 bp in length
             34633; gap of 100 bp 35334; contig of 701 bp in length 35434; gap of 100 bp in length 36127; contig of 693 bp in length
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55412: contig of 681 bp in length
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42606: contig of 695 bp ir
7706: gap of 100 bp
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50619: contig of 704 bp
19: gap of 100 bp
51404: contig of 685 bp
of 701 bp
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gap of 10
87: contig of 7
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45782: contig c
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36921: contig
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Query Match 12.1%; Score 243.6; DB 2; Length 61101; Best Local Similarity 53.6%; Pred. No. 8.2e-46; Matches 444; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

ggtatgcaaatgtagccaataatactcaaactcctgggctcaagcgatcctcccacct 730

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Qy 851 ttattttgtcatttagagttcataaatattagggtttattttctaaatagaatagtttaa 910

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RESULT 13
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DEFINITION Homo sapiens 3q27 BAC RP11-410F19 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
ACCESSION AC009247
ACCESSION AC009247
REYWORDS
HTG.
SOURCE
human
ORGANISM Homo sapiens
Craniata: Vertebrata: Euteleostom1:

REFERENCE I (bases I to 14637).

REFERENCE I (bases I to 146376)

AUTHORS MUZDA, D. Adams, C., Balley, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Banley, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Duydan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganesh, R., Garcia, D.K., Gorrell, J.H., Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Laall, B., Lil, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R., Moore, S., Moorish, T., Morgan, M., Morris, S., Nash, S., Nash, S., Nashon, S., Payton, B., Perez, L., Pull, L., Oulles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T.,

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1371. .1711
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                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley.K.C.
Direct Submission
Submitted (30-MAR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 146376)
                                                                                                                                                                                              Submitted (08-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 146376)
                                                                                                                                                                                                                                                                                                                                                  Submitted (08-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 146376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 14, 2001 Lils sequence version replaced gi:13489132. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S.,
Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J.,
Wrensford,G., Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANNOTATION OF FEATURES:
                                                                                                                              (bases 1 to 146376)
                                                                               Direct Submission
                                                                                                                                                    Worley, K.C.
Direct Submission
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Direct Submission
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Direct Submission
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html.
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repeat_region

repeat_region

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Location/Qualifiers

QUALSTAT-REPORT

FEATURES

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repeat_region

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Direct Submission
Submitted (10-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louls,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
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1: contig of 1170 bp in length
1: gap of unknown length
2: contig of 1219 bp in length
3: contig of 1219 bp in length
3: contig of 1038 bp in length
4: gap of unknown length
5: contig of 1239 bp in length
7: gap of unknown length
7: gap of unknown length
8: contig of 1201 bp in length
9: contig of 1201 bp in length
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contig of 1547 b
gap of unknown l
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gap of unknown l
contig of 1290 b
gap of unknown l
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                                The sequence of Homo sapiens clone
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22426:
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Waterston, R.H.
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1 (bases 1 to 22426)
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                     Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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complement(21253. 21311)
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20758. 20865
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0276. .20580
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HTG; HTGS_PHASE1.
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AL359540 149916 bp DNA linear HTG 08-FEB-2002 Homo sapiens chromosome 1 clone RP4-534D1 map p34.1-35.3, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Submitted (07-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk humquery@sanger.at.uk clone requests: clonerequest@sanger.ac.uk on Jan 19, 2002 This sequence version replaced gi:16944918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                      10775 TTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 10716
10954 ATTATGTTATATTATATATTTTTTTTGAGACAGGGTCTCACTCTATTGCCCAGGCTGG 10895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Blyg Dye; 100% of reads
Consensus quality: 149780 bases at least Q40
Consensus quality: 149824 bases at least Q30
Consensus quality: 149855 bases at least Q20
Insert size: 149916; sum-of-contygs
Insert size: 150837; 6.6% error; agarose-fp
Quality coverage: 9.27x in Q20 bases; sum-of-contigs Quality
coverage: 9.22x in Q20 bases; agarose-fp
                                        agtgcagtggcacaatctcggctcattgcaacctccgcctcccgcgttcaagtgattctc
                                                        tttgtatttttagtagagacggggttttccacgttggccgggctggtctcaaactcttg
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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1. 149916
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Pred. No. 1.8e-45;
0; Mismatches 405; Indels
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 107819)
DOE Joint Genome Institute.
Direct Submission
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Submitted (28-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 107819)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 8, 2001 this sequence version replaced gi:13470140.

Praft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 140734)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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DOE Joint Genome Institute.
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1 (bases 1 to 140734)
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Homo sapiens
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                                                                                                                                                                                     Length 140734;
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                   Genome Institute
Drive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:134
Draft Sequence Produced by DOE Joint Genome Institut
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                       Indels
                                                       Sednence;
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                                                                                                                                                                                     6
                                           www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Seq
Estimated Total Number of Errors is 0.3.
STS Content:
SHGC-64113 G38695.
                                                                                                                                                                                      DB
                                                                                                                                                                                    Score 1259; DE
Pred. No. 0;
0; Mismatches
                                                                                                                                     /clone="CTD-2202K16"
28409 c 28508 g 40553
                                                                                                           /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                         Location/Qualifiers
1. .140734
                                                                                                                              /chromosome="5"
                                                                                                                                                                                     62.4%;
99.9%;
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DNA linear HTG 20-APR-2001
CTD-2201J22, WORKING DRAFT
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                                         ggtaagagcccagtagtgttcataagaagccaatagagagcaggagccactttatcaggt
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                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Consensus quality: 131953 bases at least Q40
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Homo sapiens chromosome 5 clone
SEQUENCE, 9 unordered pieces.
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Mammalia, Eutheria, Primates, C
1 (bases 1 to 14337)
DE Joint Genome Institute.
Sequencing of Human Chromosome
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Center Code: JGI
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Center Project Name: 704971
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DOE Joint Genome Institute.
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AC022132.5 GI:13699628
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Consensus quality: 137362 bases at least Q20
Estimated insert size: 119000; pulse field gel estimation
Estimated insert size: 142572; sum-of-contigs estimation
Quality coverage: 7.17 in Q20 bases; pulse field gel estimation
Quality coverage: 5.98 in Q20 bases; sum-of-contigs estimation
* ROTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the places
* is not known and their order in this sequence record is
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                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1309; Conservative 0; Mismatches

    .143372
/organism="Homo sapiens"
/db_xref="taxon:9606"

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mRNA linear PRI 27-SEP-2000 epithelial chemokine mRNA, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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        AF266504 768 bp
Homo sapiens mucosae-associated
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AF266504.1
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/translation="MOORGIAIVALAVCAALHASEAILPIASSCCTEVSHHISPRLLE
RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
                           PRI 02-JAN-2001
                                                                                                               Submitted (01-DEC-1998) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnolog Institute, 800 Xiangyin Road, Shanghai 200433, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTGGATGAAAGTGCAAGCTGCCAAGAAAAATGGTAAAGGAAATGTTTGCCACAGGAAG 360
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                      1349 bp mRNA linear
Homo sapiens CCK1 protein (CCK1) mRNA, complete cds.
AF110384
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                                                                                                                                                                     Zhang, W., He, L., Yuan, Z., Wan, T. and Cao, X. A novel CC chemokine homology with TECK Unpublished 2 (bases 1 to 1349) Zhang, W., He, L., Yuan, Z., Wan, T. and Cao, X. Direct Submission
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100.0%; Pred. No. 3.2e-261;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
1. .1349
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/db_xref="G1:12002127"
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/gene="CCK1"
/note="similar t
                                                                      AF110384.1 GI:12002126
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       1 (bases 1 to 768)
Pan, J., Kunkel, E.J., Gosslar, U., Lazarus, N., Langdon, P.,
Broadwell, K., Vierra, M.A., Genovese, M.C., Butcher, B.C. and Soler, D.
Cutting edge: A novel chemokine ligand for CCR10 and CCR3 expressed
by epithelial cells in mucosal tissues
J. Immunol. 165 (6), 2943-2949 (2000)
                                                                                                                                                                                                                                                                                                                                  /protein_id="AaG16691.1"
/db_xref="G1:10312152"
/tb_xref="G1:10312152"
/tb_xref="G1:10312152"
/ranslation="MQGRGLAIVALAVCAALHASEAILPIASSCCTEVSHHISRRLLE
RVNWCRIQRAGGDGLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
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/product="mucosae-associated epithelial chemokine"
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                                                                                                                           2 (bases 1 to 768)
Gosslar,U., Pan,J., Kunkel,E.J. and Butcher,E.C.
Direct Submission
Submitted (UnAr-2000) Department of Pathology, Stanford
University, 3801 Miranda Ave, Palo Alto, CA 94304, USA
Catarrhini; Hominidae; Homo
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100.0%; Pred. No. 3.2e-261;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="5"
53. 436
                                                                                                                                                                                                                                                                                         /note="chemokine; MEC"
Mammalia; Eutheria; Primates;
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Papsidero,L.D., Dyster,L.M. and Frustaci,J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 6 23-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.5%; Score 313; DB 6; Lø
Best Local Similarity 100.0%; Pred. No. 3.3e-160;
Matches 313; Conservative 0; Mismatches 0;
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                                                                                                                                                                                         AR174328 3117 bp
Sequence 6 from patent US 6306653.
AR174328
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582 c 566 q
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1 (bases 1 to 381)
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Homo sapiens CC chemokine CCL28 (SCYA28) mRNA, complete cds.
AF220210
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RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                        Wang, W., Soto, H., Oldham, E.R., Buchanan, M.E., Homey, B., Catron, D. Jenkins, N., Copeland, N.G., Gilbert, D.J., Nguyen, N., Abrams, J., Kershenovich, D., Smith, K., McClanahan, T., Vicari, A.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAX Research Institute,
                                                                                                                                                                                                                                                                                                                                   Identification of a novel chemokine (CCL28), which binds CCR10
J. Biol. Chem. 275 (29), 22313-22323 (2000)
20357357
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512 cataaaactccttattagagagtctacagataaaatctacagagacaattcctcaagtgga
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Soto, H., Vicari, A. and Zlotnik, A.
Soto, E., Vicari, A. and Zlotnik, A.
Submisted (Jo-DEC-1999) Immunobiology, DN
California Ave, Palo Alto, CA 94304, USA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .384
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1 (sites)
Yound, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                              PAT 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  gcatttaattttatttttcctgacatttctgcaagctttgtatttatatttccacttt 1812
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Patent: WO 0194629-A 5359 13-DEC-2001
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/db_xref="taxon:9606"
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, 2.
Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Papsidero,L.D., Dyster,L.M. and Frustaci,J.M. Detection and treatment of breast disease Patent: US 6306653-A 7 23-OCT-2001; Location/Qualifiers 1.381
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Best Local Similarity 100.0%; Pred. No. 8e-128;
Matches 254; Conservative 0; Mismatches 0;
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Pred. No. 1.5e-141;
0; Mismatches 2;
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Sequence 175 from Patent WO0194629.
AX329666.1 GI:18102644
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74 c 79 g 17
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129427 bp DNA linear HTG 23-APR-2001 bno sapiens chromosome 19 clone CTD-2223D2, WORKING DRAFT SEQUENCE, 11 ordered pleces.
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      745 actgggattataggtgtgagccacagtgcctggcctaattattttcttgtgatcaaattc 804
                     104 ACTGGGATTATAGGTGTGAGCCACAGTGCCTGGCCTAATTATTTTCTTGTGATCAAATTC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 2939 bp in length
gap of unknown length
contig of 7967 bp in length
gap of unknown length
contig of 9601 bp in length
                                                       805 aggittaatgittitggitaagaatticctacgigaatticgigt 848
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ACO20929.4 GI:13752692
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                      44 AGGTTTAATGTTTTGGTTAAGAATTTCCTACGTGAATTCGTGT 1
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Center clone name: CITB-H1_2223D2
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Unpublished
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Mammalia; Eutheria; Primates;
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Direct Submission
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     PAT 17-DEC-2001
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1 (bases 1 to 104)
Papsidero, L. D., Dyster, L.M. and Frustaci, J.M.
Detection and treatment of breast disease
Patent: US 6306633-A 8 23-OCT-2001;
Location/Qualifiers
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Papsidero, L. D., Dyster, L.M. and Frustaci, J.M. Detection and treatment of breast disease
Patent: US 630663-A 11 23-OCT-2001;
Location/Qualifiers
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Pred. No. 2.8e-99;
0; Mismatches 2;
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311 bp 1
Sequence 11 from patent US 6306653.
AR174333
AR174333.1 GI:17914653
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24 c 15 g
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99.3%;
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Query Match

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Silvano, S., Baldwin, J., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouklagalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferretra, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McClark, A., McKernan, K., McPheeters, R., Marquis, M., McEwan, P., McClark, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stoyanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vasalliev, H., Viel, R., Wux, Wyman, D., Ye, W.J.,
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                  121814: contig of 12185 bp in length 121914: gap of unknown length 124923: contig of 3018 bp in length 125032: gap of unknown length 129427: contig of 4395 bp in length.
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o. 1.1e-25;
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/db_xref="taxon:9606"
/chromosome="19"
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Matches 68; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                             Center clone name: 384_E_6
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145359 bases at least Q30
Consensus quality: 155420 bases at least Q30
Consensus quality: 159351 bases at least Q30
Insert size: 161352; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
            Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L5880
                                                                                                                                                                                                                                                                                                                                                                                                              of 100 bp contig of 1296 bp in length
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contig of 1540 bp in length
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contig of 1732 bp in length
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contig of 1710 bp in length
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contig of 2033 bp in length
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51: gap of 100 bp
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51475: contig of 4288 bp in length
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contig of 4518 bp in length
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79365: contig of 4997 bp in length
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contig of 4500 bp in length
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contig of 4821 bp in
Web site: http://www-seg.wi.mit.edu
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contig of 3448 bp
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in length

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83212 83311: gap of 100 bp 83312 88101: contig of 4790 bp in length 88102 88201: gap of 106 bp 88202 93786: contig of 5584 bp in length 93786 93885: gap of 100 bp 100 bp 100508 100507: contig of 6522 bp in length 100408 100507: gap of 100 bp 100508 108158: contig of 7651 bp in length 108159 108288: gap of 100 bp 115532 115731: gap of 100 bp 115532 115731: gap of 100 bp 115538 125488: contig of 7373 bp in length 115732 125488: contig of 9757 bp in length 125589 136013: contig of 100 bp 125588: gap of 100 bp 136013: gap of 100 bp 136113: gap of 100 bp 136113: gap of 100 bp 136111 149210: contig of 12997 bp in length 149111 149210: contig of 12542 bp in length 149111 149210: contig of 15442 bp in length.
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Direct Submission

Submitted (25-APR-2000) Human Genomic Center, Institute of Genetics. Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P. R.China

3 (bases 1 to 172805)

5 Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,Y., Li,Y., Li,Y., Li,Y., Li,Y., Li,Y., Li,Y., Li,W., Li,Y., Li,Y., Li,Y., Li,W., Li,Y., Wing,J., Wang,J., Wang,Y., Zhang,X., Zhu,B., Zhu,B.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172805)
Xiong, H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y.,
Cai, Z., Ying, H.F., Wang, H., Gu, W., Zhu, G., Tu, Y., Zhang, X., Jia, J.,
Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
Chen, Z., and Huang, M.
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Unpublished
2 (bases 172805)
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Homo sapiens chromosome 3 clone RP11–785A7 map 3p, complete
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ACO66608.5 GI:12745084
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Best Local Similarity 100.
Matches 68; Conservative
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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100101, P.R.China

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On Feb 11, 2001 this sequence version replaced gi:8101281.
                                             Center:Beijing Center
Center code:Beijing
Website:http://www.genomics.org.cn
http://www.genomics.org.cn
http://www.genomics.org.cn
Contact:hgc@ligtp.ac.cn
Contact:hgc@ligtp.ac.cn
Center project name:1% project
Center project name:1% project
Center clone name: RP11-785A7
Center clone name: RP11-785A
Sequencing vector: prof18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 17621 bases at least Q30
Consensus quality: 17621 bases at least Q30
Consensus quality: 17621 bases at least Q30
Unsert size: 172805; sum-of-contigs
Quality coverage: 8.12x in Q20 bases; sum-of-contigs
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Best Local Similarity 100.0%; Pred. No. 3.7e-25;
Matches 67; Conservative 0; Mismatches 0; Indels
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53766 a 33397 c 32927 g 52715 t
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1.172805
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/db_xref="taxon:9606"
/chromosome="3"
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Source
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ORIGIN
   COMMENT
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Search completed: October 7, 2002, 13:05:27 Job time: 9417 sec

Db 76891 GCCTCAT 76897 1229 ggctcat 1235

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